BD004278 Apo E hum CQ875269 Sequence CQ875269 Sequence CQ866276 Sequence CQ981476 Sequence DD166083 Treatment AR380462 Sequence AX821568 Sequence AX821568 Sequence AX821569 Fower Sequence

BC003557 Homo sapi AR51680 Sequence BC072022 Homo sapi E08423 DNA coding BD004277 Apo E hum DD166085 Treatment

Sequence 1

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JP 1985118189-A/1
25-JUV-1985
29-NOV-1983 JP 1983224980
TERANISHI YUTAKA, TAKAMATSU NOBUHIKO, MATSUI YASUSHI, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae, Homo.

1 (bases 1 to 1110)

Teranishi,Y., Takamatsu,N., Matsui,Y., Kimura,M. and Ikeda,Y.
DNA FRAGMENT
PATEMENT: JP 1985118189-A 1 25-JUN-1985;
MITSUBISHI CHEM IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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cDNA coding human apolipoprotein E3.
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strandedness: Double;
topology: Linear;
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AC145523
AC151887
BABAPOE
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AF303830
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BD004279
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AX358722
AF050154
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AR282772
MFAPOE
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BD004277
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AX409597
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HUMAPOE4
AF261280
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                                                                                                                           AR531680
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JP 1985118189-A/1.
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Homo sapiens
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91.7 107567
91.3 3805
91.3 3805
91.3 5515
90.5 5515
88.6 5413
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85.1 183798
84.0 191327
83.1 4762
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PN 0P 198511
PD 25-UN-19
PF 29-NOV-19
PI TERANISHI
KIMURA MASAKO,
PI IKEDA YASI
PC C12N15/00
CC strandedn
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ACCESSION
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KEYWORDS
SOURCE
ORGANISM
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
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Command line parameters:
-MODEL=frame+_D2n.model -DEV=xlh
-MODEL=frame+_D2n.model -DEV=xlh
-Q=Abss/ABSWEBE spool/10509827854/runat_14062006_081825_26727/app_query.fasta_1
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-NO MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -KGAPOP=10 -KGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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E00823 DNA sequenc
AX302545 Sequence
                                                                          June 14, 2006, 19:02:13; Search time 9258.62 Seconds (without alignments) 3097.698 Million cell.updates/sec
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                                                                                                                                                 1 KVEQAVETEPEPELRQQTEW.....VEKVQAAVGTSAAPVPSDNH 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
        GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                     - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                6366136 seqs, 31973710525 residues
                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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E00823
AX302545
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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length: 2000000000
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gb_om:*
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Database :

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Minimum DB e Maximum DB e

Scoring table:

Perfect score:

Sequence:

OM protein

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AX333278 Sequence
AX409597 Sequence
M12529 Human apoli
BD064748 Method fo
BD064279 Apo E hum
CQ719977 Sequence
BD064811 Diagnosis
AF261279 Homo sapi
AX35872 Sequence
AF261279 Homo sapi
AX31977 Methods a
AR262772 Sequence
X13887 Monkey mRNA
DD166084 Treatment
M10065 Human apoli
AF261280 Pan trog1
AF261280 Pan trog1
AF26473 Paylobates
AC145523 Paylobates

PAT 29-SEP-1997

1493 1493 1493

Score

Result No.

AC021988 Homo sapi AF303830 Tupaia gl M29322 Baboon apol

AF200499 Pan trogl AF200502 Gorilla g

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                                    241 AlalysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg
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Matches:
Conservative:
Mismatches:
Indels:
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Location/Qualifiers
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                                                          15. .968
/product='apolipoprotein E3 precursor'
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eptide (9. .965

Location/Qualifiers

1. .1110

/organism="Homo sapiens"

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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
hypothetical: No;
anti-sense: No;
*source: tissue_type=liver;
Location/Qualifiers
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ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu
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Matches:
Conservative:
Mismatches:
Indels:
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Homo sapiens
Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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                                       AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg
                 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu
                                                                                                                                            GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis
                                                                                                                                                                                         GAGGTGCAGGCCATGGTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC
                                                                                                                                                                                                                 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu
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Tumor markers in ovarian cancer
Patent: WO 0175177-A 63 11-OCT-2001;
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Sequence 63 from Patent W00175177.
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AX302545.1 GI:17383082
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CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 474
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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                             GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis
                                               GAGGIGCAGGCCATGCTCGGCCAGAGCACCGAGAGCTGCGGGTGCGCCCTCGCCTCCCAC
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4-Oxo-quinazolines as LXR nuclear receptor binding compounds
Patent: EP 1398032-A 11 17-MAR-2004;
PheneX Pharmaceuticals AG (DE)
Location/Qualifiers
1. 1156
| /organism="Homo sapiens"
| /mol_type="unassigned DNA"
| /db_xref="taxon:9606"
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Sequence 11 from Patent EP1398032.
CQ785970 GI:45721147
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2 Pujita, S., Hamanaka, H., Fukui, Y. and Yokoyama, M.

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B Atenti JP 201017028-A 2 23-JAN-2001;

P J 23-JAN-2001

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P P 23-JAN-2001

P P 23-JAN-2001

P P 24-APR-2000 JP 2000128919

P R SHINOBU FULITA, HIROKI HAMANAKA, YUKO FUKUI, MINESUKE YOKOYAMA PC
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    ..1156
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"

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JP 2001017028-A/2.
Homo sapiens (human)
Homo sapiens
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Apo E humanized mammal.
BD004278
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Herr, A., Hinzmann, B., Dahl, E., Staub, E., Pilarsky, C. and Specht, T. Human nucleic acid sequences from carcinomas of the bladder Patent: WO 2004076613-A 12 10-SEP-2004; Herr, Alexander (DE); Hinzmann, Bernd (DE); Dahl, Edgar (DE); Staub, Eike (DE); Pilarsky, Christian (DE); Specht, Thomas (DE) Location/Qualifiers
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/db_xref="taxon:9606"

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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                       GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu
                                                                                            GInLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla
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                                         GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal
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Sequence 12 from Patent CQ875269
CQ875269.1 GI:52748357
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281 GlubyaserTrpPheGlubroiew(a)Glubroiew(a)Glubroiem(a) 280 GCCAAAACTOCTCCACCCCCCTCCACCCCCCCCCCCCCCC	101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 115 CAGGCCGGCTGGGGGGGGGACATGGAGGGGGGGGGGGGG

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                           LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla
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Cocks B.G., Stuart, S.G. and Seilhamer, J.J.
Cocks B.G., Stuart, S.G. and Seilhamer, J.J.
Compositions for the detection of blood cell and immunological response gene expression
Patent: US 6607879-A 1007 19-AUG-2003;
Incyte Corporation; Palo Alto, CA
Location/Qualifiers
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                                           GTGTACCAGGCCGGGGGCCCGCGAGGGCCCGGCGCCTCAGCGCCTTCAGCGCGCCATCCGCGAGCGC
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1 (Dases 1 to 1156)

1 shida,B. Kern,J., Duncan,K., Bailey,C. and Schwartz,D.M.

Treatments for Age Related-Macular Degeneration

1 THE REGENTS OF THE UNIVERSITY OF CALIFORNIA

OS Human

PP 28-APR-2005

PP 06-DEC-2002 UP 2003550736

PR 03-OGT-2002 US 60/415864,07-DEC-2001 US 60/340498 PI brian ishida,john kern,keith duncan,cathy bailey,daniel m PI cC C C FH Key
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                                                                 Treatments for Age Related-Macular Dogeneration.
DD166083
DD166083. GI:83962539
JP 2005511713-A/1.
Homo sapiens (human)
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    /organism="Homo sapiens"
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Patent: WO 03068986-A 1 21-AUG-2003;
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And E is located on chromosome 19 --Jackson, Bruns and Breslow, PNAS USA 81, 2945-2949 (1984) -- and is believed to be linked to the Apo C-II gene (see separate entry).

The two mutations causing type III hyperlipoproteinemia (apolipoprotein E phenotype E3/3) produces substitutions of Arg for Cys at amino acid Il2 and Cys for Arg at amino acid position 142.

Draft entry and printed copy of sequence for [1] kindly provided by L.L. Gill, University of Aberdeen.

Complete source information:

Human liver [1], [J. Biol. Chem. 258, 11422-11422 (1983)], [2], [3], [4] and blood [5], cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /Godon_start=1
/product="preapolipoprotein E"
/protein_id="Aab59546.1"
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/db_xref="G1:178851"
/db_xref="G1:178851"
/db_xref="G1:178851"
/translation="MKVLMAALLVTFLAGGGAKVEQANETEPEPELRQGTEWQSGQRW
ELALGREWDYLRWOTLSEQYQEELLSSQVTQELRALMDETWKELKAYKSELEEQLTP
VAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAMLGQSTRELRYRLASHLR
KLRKILLRADDDLQKRLAYQAGAREGABRGLSAIRBRLGPLVEQGRVRAATVGSLAG
QPLQERRQAMGSRLARAMEERWGSRTRORLDSVKEQVAEVRALLEEQAQQIRLQABAFQ
ARLKKWPEPLVEDMQRQWAGLVEKVQAAVGTSAAPVPSDNH"
see the separate entry.
[J. Biol. Chem. 258, 11422-11422 (1983)] is too extensively revised relative to [1] to record the revisions in the FEATURES table. The sequence below is that of [J. Biol. Chem. 258, 11422-11422 (1983)] and [3].
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/db_xref="taxon:9606"
/map="19q13.2"
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/note="in variant"
/citation=[4]
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Homo sapiens preapolipoprotein E (APOE) mRNA, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 (bases 577 to 624) (dill.L., Peoples, O.P., Pearston, D.H., Robertson, F.W., Humbhries, S.E., Cumming, A.M. and Hardman, N. Isolation and characterisation of a variant allele of the gene for human apolipoprotein E
                                                                                                                                                                                             apolipoprotein; apolipoprotein E; lipoprotein; polymorphism; very
low density lipoprotein.
Homo sapiens (human)
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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1 (bases 355 to 1156)

1 (bases 355 to 1156)

1 (bases 1.L., McPherson, J., Nussbaum, A.L., Williams, H.W.,
Lofquist-Kahl, F., Karathanasis, S.K. and Zannis, V.I.

Identification and DNA sequence of a human apolipoprotein E cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthesis, intracellular processing, and signal peptide of human
  GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCCCCTGTGCCCCAGCGACAATCAC 1011
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    corrected in [J. Biol. Chem. 258, 11422-11422 (1983)]. [J. Biol. Chem. 258, 11422-11422 (1983)] correction of [1]. [4] epsilon-3 and variant.
    epsilon-2 allele.

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Rall,S.C. Jr., Newhouse,Y.M., Clarke,H.R., Weisgraber,K.H.,
McCarthy,B.J., Mahley,R.W. and Bersot,T.P.
Type III hyperlipoproteinemia associated with apolipoprotein E
phenotype E3/3. Structure and genetics of an apolipoprotein E3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wallis S.C., Rogne, S., Gill, L., Markham, A., Edge, M., Woods, D., Williamson, R. and Humphries, S.
The isolation of cDNA clones for human apolipoprotein E and the detection of apoE RNA in hepatic and extra-hepatic tissues EMBO J. 2 (12), 2369-2373 (1983)
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McLean, J.W., Elshourbagy, N.A., Chang, D.J., Mahley, R.W. and
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J. Biol. Chem. 259 (10), 6498-6504 (1984)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases; Homo.

2 (bases; Lo. 186)

3 Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

3 Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

3 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schamer, C.M., Schuler, G.D.,

3 Altschul, S.F., Jordan, H., Morce, T., Max, S.I., Wang, J., Hsieh, F.,

4 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

5 Capteron, M., Soares, W.M. B., Bonaldon, F., Casavant, T.L.,

5 Chetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

6 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

7 Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

8 Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

7 Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

8 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

8 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schuutz, J., Myers, R.M.,

8 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Sanilus, D.E.,

8 Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

8 Proc. Natl. Acad. Sci. U.S., 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1186 bp mRNA linear PRI 29-JUN-2004
Homo sapiens apolipoprotein E, mRNA (cDNA clone MGC:1571
IMAGE:3355712), complete cds.
BC003557.1 GI:13097698
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LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly
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                                                                                 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA
                                                                                                                              ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg
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and [4] variant; a in [4]'normal'"
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/citation=[4]
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Kaser, M.R.
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QPLQERAQAWGERLERARMEERMSTRRRLDEVKEQVAEVRAKLEEQAQQIRLQABAFQ
ARLKSWFEPLVEDMQRQWAGLVEKVQAAVGTSAAPVPSDNH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 6 Row: h Column: 23
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4557324.

Location/Qualifiers
                                                                                                                                                                                                                                                                                       Andy Chan, Steve S. Chand, Milliam Chow, Alison Cloutier, Ruth Reatherstone, Malachl Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Parvane Nasedi, JR Santos, Angelique Schnerch, Ursula Skalska, Buane Smallus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Aslm Siddiqui, Rob Holt, Marco Marra.
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                                     Direct Submission
Submitted (20-FEB-2001) National Institutes of Health, Mammalian
Submitted (20-FEB-2001) National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                          NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATD in The
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
BNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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Human; antilipaemic; neuroprotective; nootropic; genetic variant; APOE; apolipoprotein B; haplotyping; familial dysbetalipoproteinaemia; therapy; genotyping; type III hyperlipoproteinaemia; Alzheimer's disease; SNP; atherosclerosis; single nucleotide polymorphism; chromosome 19q13.2; ss.
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C adent for treating a specific condition or disease predicted to be associated with APOE activity and in the design of clinical trials of candidate drugs for treating a specific condition or disease predicted to be associated with APOE activity. Genotyping or haplotyping methods are useful to screen for compounds targeting APOE to treat a specific condition or disease predicted to be associated with APOE activity. Genotyping or haplotyping methods are cuseful to screen for compounds targeting APOE to treat a specific condition or disease associated with APOE activity. The present sequence condition or disease associated with APOE activity. The present sequence is a cDNA encoding human APOE protein. APOE gene is located on chromosome
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                                                          replace (388, C)
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P-PSDB; AAE15158.
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Best Local Similarity:
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The encoded protein is used to treat subjects who are deficient in apolipoprotein-E (or who produce abnormal forms of this molecule) and therefore are likely to suffer from hyperlipidemia, resulting in arteriosclerosis. It can also be used to raise antisera for detecting the protein deficiency or production of abnormal forms. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                  GCCAAGCTGGAGGAGCAGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC
               LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly
                                   GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu
                                                                                               MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg
                                                                                                                                                                                                          AlaLysteuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg
                                                                                                                                                                                                                                                                        LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal
                                                                                                                                                                                                                                                                                                       CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCCAGTGGGCCGGGCTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New DNA sequence coding for human apolipoprotein-E - and expression vectors and transformed cells contg. it.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Apolipoprotein-E; hyperlipidemia; arteriosclerosis; ss.
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15. .968
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(first entry)
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                                                                                                                                                                                                                                                                    The invention relates to a new microarray which comprises probes for genes involved in psychoneuroendocrinimmune (PNI) activity. The microarray is useful in diagnosing a condition associated with PNI activity, such as CFS, type-2 diabetes, allergic condition, inflammation, cancer and infection. The present sequence represents a psychoneuroendocrinimmune gene expressed sequence tag. Note the specificatio mentions SEQ ID NO of up to 3314 but only sequences up to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 174
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                                                                                                                                                         New microarray comprising probes for genes involved in psychoneuroendocrinimmune (PNI) activity, useful in diagnosing condition associated with PNI activity, e.g., inflammatory or i
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 954 BP; 168 A; 290 C; 377 G; 119 T; 0 U; 0 Other;
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Matches:
Conservative:
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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The invention relates to methods for diagnosing and prognosing ovarian tumours in an individual via the detection and measurement of the expression of covarian tumour marker genes (ABA83103-ABA83162, ABA83180, ABA83181 and ABA83184) or segments thereof (ABA83103-ABA83162, ABA83180, ABA83181 and ABA83184) or segments thereof (ABA83103-ABA83169, ABA83181) and ABA83183). The methods of the invention are useful for assessing the relative severity of ovarian cancer, in prognostic tests for assessing the relative severity of ovarian cancer, in tests for conitoring a patient in remission from ovarian cancer, in tests for monitoring a patient in remission from ovarian tumour selected for ovarian tumour file. The methods can additionally be used to identify a particular tumour as serous cystadenoma, borderline serous tumour, serous cystadenoma, borderline serous tumour, mucinous cystadenoma, borderline serous tumour, mucinous cystadenoma, borderline mucinous tumour, mucinous cystadenoma, cystadenofibroma, adenofibroma and Brenner tumour. The ovarian tumour marker genes of the invention were identified tumour. The ovarian tumour marker genes of the invention were identified coverexpressed in a broad variety of ovarian epithelial tumour cells coverexpressed in a broad variety of ovarian epithelial cells. The marker genes are membrane implicated in immune response pathways, in the regulation of cell collised or secreted. In addition to their use as diagnostic and
                                                                                                                              Ovarian tumour marker gene; human; overexpression; upregulation; epithelial tumour; cancer; diagnosis; prognosis; disease monitoring; identification; serous cystadenoma; borderline serous tumour; serous cystadenocarcinoma; mucinous cystadenocarcinoma; mucinous cystadenocarcinoma; mucinous cystadenoma; borderline mucinous tumour; endometrioid carcinoma; undifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma; adenofibroma; Brenner tumour; serial analysis of gene expression; SAGE; immune response pathway; cell proliferation regulation; protein folding; membrane localised; secreted; therapeutic target; cytostatic; gene therapy; vaccine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting and identifying ovarian tumor, identifying increased risk for developing ovarian cancer, and determining effectiveness of ovarian cancer treatment, by measuring expression level of ovarian tumor marker
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                                                                                      Apolipoprotein E ovarian tumour marker gene, SEQ ID NO:63
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The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide gray acquences (TAT) nucleic acid comprising: (b) the full-length coding region of sequence (1a) (c) the complement of (a) or (b); (d) a sequence that has 80% (a). (c) the complement of (a) or (b) a sequence that hybridises to (a)-(c). Also described: (1) an expression vector comprising the above expression vector. (a) process for producing a polypeptide; (4) an isolated polypeptide comprising: (a) an amino acid sequence encoded by the full-comprising: (a) an amino acid sequence encoded by the full-comprising at least 80% identical to (b); (s) a chimaric polypeptide; (c) a variety of the above polypeptide fused to a heterologous polypeptide; (d) a chimaric polypeptide; (e) an isolated antibody that binds to the above polypeptide; (d) a primaric polypeptide; (e) a composition of matter comprising the above polypeptide; (a) a chimaric polypeptide; (b) a tumour-associated antipody, oliopeptide or TAT binding organic molecule; in combination antibody, oliopeptide or TAT binding organic molecule, in combination (with a carrier; (11) an article of manufacture comprising a container and the growth of the cell is at least in part dependent upon a growth of potentiating effect of the above protein; (13) a method of inhibiting the above protein; (13) a method of chimarically treating a mammal having a cancerous tumour comprising the above protein; (14) a method of a tumour in a disperence of a protein in a sample suspected of containing the above protein; (15) a method of a tumour of protein, and (17) a method of binding an antibody, oliopeptide or a call that expresses the above protein; (14) a method of a tumour of protein, and (17) a method of binding an antibody, oliopeptide or a call that expresses the protein described above; (15) methods of dispension or activity of the above protein and (17) a method of binding an antibody, oliopeptide or a call that expresses the above protein 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reventing or treating cancer. The composition is also used for preparing medicament for the therapeutic treatment or diagnostic detection of a sill proliferative disorder or cancer. The present sequence represents a
                                                                                                                        TAT; cytostatic; gene therapy;
                                                                               tumour-associated antigenic target (TAT) cDNA sequence #3836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer
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                                                                                                                     human; tumour-associated antigenic target; cancer; cell proliferative disorder; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 3836; 5504pp; English.
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Sequence 1154 BP; 208 A; 367 C; 431 G; 148 T; 0 U; 0 Other;

ADQ86961 standard; cDNA; 1154 BP

ADQ86961 ID ADQE XX RESULT 5

ApoE3"

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apoE humanized mammalian cell useful for screening for agents useful treating or preventing Alzheimer's disease and arteriosclerosis.
                                                          Human; ApoE3; Alzheimer's disease; arteriosclerosis;
                                                                                               ocation/Qualifiers
                                                                                                                                                                                               99JP-00125647.
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                                           Human ApoE3 coding sequence
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P-PSDB; AAB80997.
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Best Local Similarity:
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        Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                         The present invention relates to an ApoE humanised mammalian cell. The present sequence is the coding sequence for human ApoE3, which was used in the metchod of the present invention. The ApoE humanised mammalian cell can be used for screening for agents useful for treating or preventing Alzheimer's disease and arteriosclerosis
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Matches:
Conservative:
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Disclosure; Page 13-14; 22pp; Japanese
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                                                                                                                                                                                                                                                                                               GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
                        GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu
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                                                        LeukrgLysLeukrgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla
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                                                                                        ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg
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The invention comprises methods of detecting the presence or absence of at least one allelic variant of a polymorphic region of a gene associated with cardiovascular disease. The invention specifically relates to detecting the region of a cytochrome C oxidase subunit VID (COX6B) gene that is associated with high serum cholesterol, or the region of the Necetylglucosaminy! Transferase component glycosylphosphatidylinositol-1 (GPI-1) gene that is associated with low serum high density lipoprotein (HDL). The methods of the invention are useful for detecting a predisposition to high serum cholesterol, low serum HDL and readiovascular disease. The methods are also useful for elucidating pathological pathways, developing diagnostic assays and new drug theraptes for such disorders. The present DNA sequence represents a human cardiovascular disease
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                                                                                                           Detecting the presence or absence of an allelic variant of a polymorphic region of COX6B and/or GPI-1 gene, useful for detecting a predisposition to high serum cholesterol, low serum HDL and cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40
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Conservative:
Mismatches:
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Kleyn PW;
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The present sequence is a human apolipoprotein E (apoE) isoprotein, apoE3 DNA. The apoE lipoproteins are useful for lowering cholesterol, delaying the onset of atheroselerosis, treating or regressing atheroselerosis without inducing hypertriglyceridaemia, in a mammal lacking an endogenous, normally functioning apoE gene or low density lipoprotein (LDL) receptor or is at risk for developing atheroselerosis due to accumulation of lipoprotein remnants in the bloodstream or having a defect in remnant removal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New apolipoprotein E polypeptide and nucleic acid, useful for lowering cholesterol, delaying the onset of or treating atherosclerosis in mammal, without inducing hypertriglyceridemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
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Matches:
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Mismatches:
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                                                                       Claim 14; Page 81; 91pp; English
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                                                                                                                         GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu
                                                                                                                                                                MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg
                                                                                                                                                                                                                ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGAGGTGCGC
                                                                                                                                                                                                                                                    AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg
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                                                                                                                                                                                                                                                                                                                  CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCCAGTGGGCCGGGCTGGTG
                CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA
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                                                                                                LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly
 LeuArglysLeuArglysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla
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115. 1011
/product= "Mature human apoE isoprotein, apoE3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; apolipoprotein E; apoE; cholesterol; atherosclerosis; hypertriglyceridaemia; low density lipoprotein; LDL; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61. 1014
/*tag= a
/product= "Human apoE isoprotein, apoE3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human apolipoprotein E (apoE) isoprotein, apoE3 DNA
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04-OCT-2000; 2000US-00679088
05-APR-2001; 2001US-00827854.
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UNIV BOSTON.
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The invention relates to a mammalian cell receptor, useful in the treatment of cancer, which binds to tumour associated lipids and induces anergy or apoptosis in the T cells and antigen presenting cells (APCs). Also included are a mammalian cell useful in the treatment of cancer where the receptor which binds tumour associated lipids and induces cellular inactivation or death is deleted or functionally deactivated, producing (MI) a tumouricidal immunocyte population in vivo in a mammal (by allowing tumour associated lipids to contact immunocytes in which receptors for immunosuppressive fatty acids, ceramides, glycolipids, sphingolipids, glycosphingolipids, phosphosphingolipids, gangilosides, sialylated glycans, lipopeptides and proteoslycolipids are inactivated or deleted), a construct useful in the treatment of cancer comprising a superantigen (SMS) nucleotide inserted into a virus, a mammalian T cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mammalian cell receptor, useful in the treatment of cancer by binding o tumor associated lipids where the binding induces anergy or apoptosis of cells and antigen presenting cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Superantigen; ds; gene; SAg; staphylococcal entérotoxin; tumour; cancer; apoptosis; gene therapy; mammalian cell receptor; cytostatic; tumour associated lipid; anergy; T cell; antigen presenting cell; APC; tumouricidal immunocyte; antitumour.
                                                                                                                                                                                                                                              GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
                                                                                                                                           ATGGGCAGCCGGACCCGCGACCTCGACGAGGTGAAGGAGCAGGTGGCGAGGTGCCG
                                                                                           GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC
MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg
                                                                      AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg
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cc receptors for the lipids are inactivated or deleted to produce a tumouricidal immunocyte population, and administering the tumouricidally activated immunocytes to the host), producing (M3) a tumouricidal lipid to population ex vivo in a mammal (by allowing a tumour associated lipids are inactivated or deleted to produce a tumouricidally activated population, and administering APCs to the host), producing a tumouricidal T cell contact T cells, in which adaptor proteins, which inhibit T cell cativated to produce a tumouricidal population of T cells, in which adaptor proteins, which inhibit T cell activated to produce a tumouricidal population of T cells, and administering the tumouricidally activated T cells to the host, or allowing a superantigen-lipid raft to contact T cells to the host, or allowing a superantigen-lipid raft to contact T cells to the host), treating (M5) cancer in a mammal (by administering a lipid binding molecule which binds immunosuppressive tumour associated lipids in vivo, producing (M5) cancer in a mammal (by administering a lipid sin vivo), producing (M5) cancer in a mammal (by administering a lipid sin vivo), producing (M5) cancer and antigen to contact immunocytes in which adaptor proteins which inhibit T cell activated) and producing (M7) at edeleted or functionally deactivated) and producing (M7) at edeleted or functionally deactivated) and producing (M7) at uncuricidal T cell population are vivo in a mammal comprisered and tumouristered as functionally deactivated) and producing (M7) at uncurist Bacterial superantigens are co-administered or administered as function constructs with anti-tumour proteins or motife. The present constructs with anti-tumour protein which are condimistered as functional functionally deactivated in a condimistered as functionally and constructs or motife. The present incorporated into a fusion construct with a superantigen. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from the US patnet office website at "segdata.uspto.gov/sequence.html?DocID=2002017551"

Sequence 1156 BP; 208 A; 368 C; 432 G; 148 T; 0 U; 0 Other;

Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similari Query Match: DB: US-09-827-854A-2 (1	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Ouery Match: DB: US-09-827-854A-2 (1-299	Alignment Scores: Pred. No.: 1493.00 Match Scores: 1493.00 Match 100.0\$ Best Local Similarity: 100.0\$ Misma Cuery Match: 100.0\$ Misma 100.0\$ Gaps: US-09-827-854A-2 (1-299) x ACA64743 (1-1156)	Length: Marches: Conservative: Mismatches: Indels: Gaps:	1156 299 0 0 0 0	
Οy	1 LysValGlu	GlnAlaValGluThro	3luProGluProGluL	LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp	20
UP 1		CAAGCGGTGGAGACAC	BAGCCGGAGCCCGAGC	115 AAGGTGGAAGCGGTGGAGCAGAGCCGGAGCCCGAGCTGCGCCAGCAGCAGCGGGTGG	174
δλ	21 GlnSerGly	GlnArgTrpGluLeu	AlaLeuGlyArgPheT	21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal	40
Db 1	175 CAGAGCGG	CAGCGCTGGGAACTGC	SCACTGGGTCGCTTTT		234
λŏ	41 GlnThrLeu	SerGluGlnValGlnC	3luGluLeuLeuSerS		09
q _Q	235 CAGACACTG	TCTGAGCAGGTGCAGC	BAGGAGCTGCTCAGCT	CAGACACTGTCTGAGGAGGAGGAGGAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG	294
δλ	61 ArgAlaLeu	MetAspGluThrMetI	cysGluLeuLysAlaT	61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu	80
QQ qq	295 AGGGCGCTG	ATGGACGAGACCATG	AAGGAGTTGAAGGCCT		354
٥٨	81 GlnLeuThr	ProValAlaGluGlu	ChrArgAlaArgLeuS	81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100	100

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355 CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGCTGTCCAAGGAGCTGCAGGCGCG GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 415 cadececederradecadadaranda de a cadececece de cadecede de cade

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GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis

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GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
presence or absence of multiple haplotypic genetic variations in a preselected region of one chromosome of a chromosome pair. The method is also useful for determining the linkage phase between two adjacent loci. The method is fast, inexpensive and provides uncomplicated determination of haplotypes in nucleic acid fragments of varying length from 25-40000 base pairs. The present sequence represents the human appolipoprotein E (apoS) coding region nucleotide sequence, which is used in the exemplification of the present invention. Human apoE is located on chromosome 19913. N. B. The present sequence is not given in the appecification, but the coding sequence of apoE is referred to in Example 3 by Genbank accession number K00396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGCCCTCATGGACGACCATGAAGGAGTTGAAGCCTACAAATCGGAACTGGAAAA
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multiple haplotypic genetic variation; polymorphism; chromosome 19q13.2;
gene; ss.
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                                                                                                                                             LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly
                                                                                                                                                                          CTGGGCCCCTGGTGGAACAGGGCCGCGTGCGGCCGCCACTGTGGGCTCCCTGGCGCCGGC
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           CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA
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Mismatches:
Indels:
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                                                              LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
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                                                                                                                                                                                                                                                                                                                                          Nuclear hormone receptor ligand; ophthalmological; cholesterol transport; lipid efflux; macular degeneration; apolipoprotein E; apo E; human; gene;
                                     894
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                                                                                                                                            955 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCCCTGTGCCCAGCGAACAATCAC 1011
                                                                                                                          GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
                GCCAAGCTGGAGGAGCAGGCCCAGCACATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC
                                                                                  CTCAAGAGCTGGTTCGAGCCCCTGGTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cholesterol transport in an ocular tissue and involves delivering at least one nuclear hormone receptor ligand. The method is used for increasing lipid efflux and reverse cholesterol transport in ocular tissue, preferably retinal pigment epithelium (RPE) and/or Bruch's membrane, in an individual afflicted with AMD or Stargardts disease (fundus flavimaculatus), and for treating macular degeneration. The present sequence represents a DNA encoding a human apolipoprotein E (GenBank Accession No. K00396)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to increasing lipid efflux from and reverse
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                                                                                                                                                                                                                                                                                                                Human apo E polypeptide encoding DNA
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03-OCT-2002; 2002US-0415864P.
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DUNCAN K.
BAILEY K.
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P-PSDB; ABR62030.
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ISHIDA B.
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(BAIL/)
(KANE/)
(ISHI/)
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                                                                                                                                                                                                       ACC84919
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The present invention describes a method (MI) for identifying a nucleotaacide in a nucleic acid by means of fluorescence resonance energy transfer (FRET). MI comprises: (a) providing a first nucleotide to be conformation at least in the portion including the nucleotide to be identified in a single-stranded confaining the nucleotide to be identified, and a first received to be identified, and a first received immediately in 3' complementary to the sequence of the first nucleic acid immediately in 3' complementary to the sequence of the first nucleic acid immediately in 3' complementary to the sequence of the first nucleic acid immediately in 3' complementary to the sequence of the first nucleic acid immediately in 3' complementary to the sequence immediately in 3' complementary to the sequence immediately in 3' complementary to the sequence immediately in 3' complementary in 4' complementary in 3' complementary in 3' complementary in 4' complementary in
                                                                             identification; fluorescence resonance energy transfer; FRET; single nucleotide polymorphism; SNP; mutation; nucleic acid polymerase; nucleic acid sequencing; human; apolipoprotein B; ApoE; chromosome 19q10.2; gene; se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying a nucleotide in a nucleic acid by means of Fluorescence Resonance Energy Transfer by monitoring the presence or absence of incorporation of the nucleotide chemically linked to the second FRBT-
                                       Human apolipoprotein E (ApoE) encoding cDNA SEQ ID NO:1.
                                                                                                                                                                                                                                                                           /*tag= a
/product= "apolipoprotein E (ApoE)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
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                                                                                                                                                                                                                             Location/Qualifiers
61. .1014
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P-PSDB; ADA14199.
(first
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encodes human apolipoprotein E (ApoE), which
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                                                                                                                                                                                                                                                                                                              GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu
             present invention. Human ApoE
                                                   C; 432 G; 148 T; 0 U; 0 Other;
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299
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Conservative:
Mismatches:
Indels:
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  sequence end
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  acids. The present sequise used in an example on chromosome 19q13.2.
                                                                                                                                Similarity:
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Best Local Similari
                                                   Sequence 1156
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                                                                                                                                                                                                             receptor; lipid-based tumour associated antigen; cytostatic; antimicrobial; gene therapy; neoplastic disease; tumour; cancer; infectious disease; apolipoprotein; ds.
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                                                                                                                                                                                                                                                    The invention relates to a composition comprising a plurality of CDNAs for detecting the altered expression of genes in an immunological cresponse. The invention also relates to a method of diagnosing or monitoring the treatment of an immunopathological condition in a sample, comprising obtaining nucleic acids from a sample, contacting the nucleic conditions to form one or more hybridisation complexes and comparising the plurality of cDNAs under conditions to form one or more hybridisation complexes with the level of the detected to hybridisation complexes with the level of hybridisation complexes with the level of hybridisation complexes correlates with the presence of an immunopathological condition. Also disclosed are an expression profile comprising a microarray and a plurality of detectable complexes and comparing comprision of target polymucleotide probes. The cDNAs are useful as hybridisable array elements in a microarray for monitoring the expression of target polymucleotides. The microarray for monitoring the diagnosis of an immunopathology, such as Crohn's disease, asthma, culcarative colitis, hyperecesinophila, irritable bowel syndrome, culcarative colitis, hyperecesinophila, irritable bowel syndrome, carcinogenicity studies, forensics or pharmacogenomics. The composition carcinogenicity studies, forensics or pharmacogenomics. The composition carcinogenic fragments. This sequence carcinogenet a human cDNA of the invention. Note: The sequence data for this patent did not form part of fram intent proponer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
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                                                                                                                                     A composition comprising a plurality of cDNAs, useful for detecting altered expression of genes in an immunological response or for diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGGTGGAGCAAGCGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 CAGAGCGCCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 208 A; 368 C; 432 G; 148 T; 0 U; 0 Other;
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                                                                                                                                                                                                                             Claim 1; SEQ ID NO 1007; SOpp; English.
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     98US-00023655
                                                                       Stuart SG,
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                                     (INCY-) INCYTE CORP
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     09-FEB-1998;
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P-PSDB; AEB86466.

Marker for screening for compounds influencing a gene or protein, for treating cartilage disorders, such as, osteoarthritis, comprises a polynucleotide or a complement to specific genes, or an antibody to its protein.

Claim 1; SEQ ID NO 13; 64pp; Japanese.

The invention relates to a novel marker for cartilage disorders. The marker consists of a polynucleotide sequence of 15 bases from the sequence of acetyl-Conzyme A acetyltransferase 1, Rev-ErbA-beta, Selenoprotein P, aquaporin 1, BMP-3b; FKS06-binding protein 1A, Selenoprotein B, acyl-coA synthetase 5, epoxide hydrolase 1, or apolipoprotein B, acyl-coA synthetase 5, epoxide hydrolase 1, or collippoprotein B, acyl-coA synthetase 5, epoxide hydrolase 1, or collippoprotein B, acyl-coA synthetase 5, epoxide hydrolase 1, or collippoprotein B, acyl-coA synthetase 5, epoxide hydrolase 1, or collippoprotein B, acyl-con properties a detection method of a cartilage disorder; a disease marker for cartilage disease containing an antibody cartilage disorder using a protein sample from the subject, or a peptide from it, and the antibody as a label; screening for a material which controls expression of one of the genes above; screening for a material which which controls the activity or function of one of the proteins; and an agent to improve or treat a cartilage disorder which contains a substance controlling expression of the genes or activity of the proteins. The markers may be used as a probe or a primer, for diagnosis of conditions such as cartilage disorder, deficient healing of fractures, or in chondrocyte transplants. The screening methods are useful for identifying therapeutic compounds. This polymucleotide sequence represents the DNA encoding apolipoprotein E of the invention.

Sequence 1156 BP; 208 A; 368 C; 432 G; 148 T; 0 U; 0 Other;

1156 299 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: 1.13e-106 1493.00 100.0% 100.0% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match:

US-09-827-854A-2 (1-299) x AEB86465 (1-1156)

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qq		CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 594
ò	161 ValTyrGlnAla	ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
q	595 GTGTACCAGGCC	GIGTACCAGGCCCGGGGCCCGCGCGCCCGAGCGCCCTCATTTTTTTT
δ	181 LeuGlyProLeu	LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
qq	655 CTGGGGCCCCTG	CTGGGGCCCCTGGTGGTGGTGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC 714
٥'n	201 GlnProLeuGlr	GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
q _Q	715 CAGCCGCTACAG	CAGCCGCTACAGGAGCGGGCCTGGGGCGAGCGGCTGCCGCGCGCG
δ	221 MetGlySerArg	MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
q	775 ATGGGCAGCCGG	ATGGGCAGCCGGACCGCGCCTGGTGTGTGTGTGTGTGTGT
٥٨	241 AlaLysLeuGlu	AlaLysLeuGluGluGluAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
qq	835 GCCAAGCTGGAG	GCCAAGCTGGAGGAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894
δλ	261 LeuLysSerTrr	LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
qa	895 CTCAAGAGCTGG	CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954
ò	281 GluLysValGln	GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
qq	955 GAGAAGGTGCAG	GAGAAGGTGCTGCCGTGGGGCACCAGCGCCCCCTGTGCCCAGCGACAATCAC 1011
Search o	completed: June 14,	2006, 19:10:42

Job time : 1035.05 secs

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UI-E-EJ0-602287404

602513830

603616028

OM protein

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Sequence:

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BG774871 602649975
BI600563 603244936
BC044785 Mus muscu
AKL59105 Mus muscu
AKL59105 Mus muscu
AKL59105 Mus muscu
AKL59404 Mus muscu
BG829472 602763768
BU194461 AGENCOURT
DN102220 1097106 M
BF967857 602287176
AKL50834 Mus muscu
BI554886 603242328
DV789745 HW LIVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cercopithecidae; Cercopithecinae; Macaca.
1 (bases 1 to 975)
Magness, C.L., Fellin, P.C., Thomas, M.J., Korth, M.J., Agy, M.B.,
Proll, S.C., Fitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST 20-JUL-2004
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11LLUMIGEN MCO_48393 Katze MMLV Macaca mulatta cDNA clone
1BIUW:18409 57 similar to Bases 755 to 975 highly similar to human
Unigene Hs.515465, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BI551475 603194314
BU190668 AGENCOURT
AK131624 Mus muscu
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CA307890 UI-H-FT1-
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BG707147 602670283
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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BF967549 602287410
BM042228 603616186
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                BU849868 B
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AK149568
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KEYWORDS
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COMMENT
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AUTHORS
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CO580643
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                                                                                    Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=\dask_ABSSWEB spool/US09827854/runat 14062006 081827 26762/app_query.fasta_1
-Q=\dask_ABSSWEB spool/US09827854/runat 14062006 081827 26762/app_query.fasta_1
-DB=EST -QFWT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOFCL=0 -LOOFEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LisT=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINIEN=0 -MAXIEN=200000000 -HOST=abss02h
-USFR=US0982784 @CGN_1 1 7986 @runat_H062006 081827 26762 -NCPU=6 -ICPU=3
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Database :

Result . 8

Minimum DB Maximum DB

602287410 AGENCOURT

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CO775017

937 bp mRNA linear EST 04-AUG-2004 ILLUMIGEN MCQ 52207 Katze MNLV Macaca nemestrina cDNA clone IBIUW.28964 5' similar to Bases 5 to 934 highly similar to human APOE (Hs.110675), mRNA sequence.
CO775017.1 GI:50976280
                                                                               220
                                                                                                                                                            MetGlySerArgThrArgAsp-ArgLeuAspGluValLysGluGlnValAlaGluValAr 240
                                                                                                                                                                                                                                   galaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaAr 260
                                                                                                                                                                                                                                                                            863
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Illumigen Biosciences Inc.
2023 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.07.21. 706 Q20 bases. Library Preparation: Prof.
Michael Katze Lab at University of Washington DNA Sequencing:
Illumigen Biosciences Inc. For further information, see
                                                                                                                                                                                 gLeulysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVa 280
                                                                                                                                                                                                                                                                                                                                           Macaca nemestrina (Fry Graniata, Vertebrata, Euteleostomi, Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mamalia; Eutheria; Euarchontoglires; Primates; Catarrhini, Cercopithecidae; Cercopithecinae; Macaca.

1 (bases 1 to 937)
Magness, C.L., Fellin, P.C., Thomas, M.J., Korth, M.J., Agy, M.B., Magness, C.L., Fitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G. an Iadonato, S.P.

Analysis of the Macaca mulatta transcriptome and the sequence divergence between Macaca and human
LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly
                                        GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu
                                                                                                     684 CAGCCGCTTCAGGAGCGGGGCCCAGGCCTTGAGTGAGCGGCTTCGCGCACGGATGGAGGAA
                                                                                                                                                                                                                                                                804 CGCCCAGCTGGAAGAACAGGGCCAGCAGATAAGCCTGCAGGCCGAGGCCTTCCAAGCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .937
/organism="Macaca nemestrina"
/mol_type="mRNA"
/strain="Indian"
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BACKWARD: CACTATAGGGCGAATTGGGTA
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Plate: CL000549 row: B column: 09
Seg primer: CCCTCACTAAAGGGAACAAAA
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      Prof.
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                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="adult"
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Site_2: BsrG I; Created from CloneMiner cDNA_Library
Construction kit (catalog #18249-029)"
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  Sequenced on 2004.07.02. 690 Q20 bases. Library Preparation: Michael Katze Lab at University of Washington DNA Sequencing: Illumigen Biosciences Inc. For further information, see
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9 9 34
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Matches:
Conservative:
Mismatches:
Indels:
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BACKWARD: CACTATAGGGCGAATTGGGTA
INSET Length: 975 Std Brror: 0.00
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PCR PRimers
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1211.00
88.3%
85.2%
81.1%
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Best Local Similarity:
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5'-TTTTTTTTTTTTTTTVN-3', size-selected
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: this is
                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Homindae; Homo.

1 (bases 1 to 1027)

1 (bases 1 to 1027)

2 NIH-MGC http://mgc.nci.nih.gov/.

2 National Institutes of Health, Mammalian Gene Collection (MGC)

3 Unpublished (1999)

4 Contact: Robert Strausberg, Ph.D.

5 Email: Gapba-rémail.nih.gov

7 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

6 CONA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

7 Toshiyuki and Piero Carninol (RIKEN)

7 CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

8 DNA Sequencing by: Incyte Genomics, Inc.

7 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

8 http://mage.llnl.gov

8 Plate: LLAM11790 row: 1 column: 09

8 High quality sequence stop: 845.

8 Location/Qualifiers

8 Location/Qualifiers
                                                      BI670367 1027 bp mRNA linear BST 12-SEP-2001
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Conservative:
Mismatches:
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BI670367.1 GI:15584600
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88.4%
80.3%
                                                                                                                                                    Homo sapiens (human)
Homo sapiens
                                                                                           mRNA sequence.
 924 TGAAAAA 930
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Site_2: BsrG I; Created from CloneMiner cDNA_Library
Construction kit (catalog #18249-029)"
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Matches:
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/cone="Indage:4860585"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab.host="Dh108 (phage-resistant)"
/lab.host="Dh108 (phage-resistant)"
/clone lib="MIH MGC 49"
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/cgcAccAG(G). Size-selected >500bp for average insert size
/cgcAccAG(G). Size-selected by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNI) BNA Sequencing by: Incytte Genomics, Inc.
Clone distribution: MGC clone distribution information of found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1718 row: b column: 10
High quality sequence stop: 817.
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Mismatches:
Indels:
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Homo sapiens
Hominidae; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Hominidae; Homo
I bases 1 to 842)
INH-MGC http://wgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                        ArgalaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu
                                AGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA
                                                                                                                              GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly
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CX165559 130 A09.gl A035 NIH MGC_258 Homo sapiens cDNA clone IMAGE:7469084 57, mRNA sequence.
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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                                                                                      LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp
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                                 US-09-827-854A-2 (1-299) x BI668318 (1-933)
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Enkaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Primates; Catarrhini; Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 909)

S NIH-MGC http://mgc.nci.nih.gov/.

Ingublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapba-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Bioscience Corporation
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2831 row: j column: 09
High quality sequence stop: 574.
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/db_xref="taxon:9606"
/clone="INAGE:659859"
/lissue_type="teratocarcinoma, cell line"
/lab_host="DH108 (phage-resistant)"
/clone_lib="NIH_MGC_109"
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OCHICLEC TORILLE S. Gerhard, Ph.D.
CONICET: Daniels S. Gerhard, Ph.D.
CONICET: Daniels S. Gerhard, Ph.D.
CONICET: Daniels S. Gerhard, MD 20892
Bmall: Gapobe-refearl: Express Genomics, Inc.
CONNALIBHORATY Preparation: Express Genomics, Inc.
CDNA Library Arrayed by: The ILM.A.G.E. CONSOTTIUM (LIMI)
DNA Sequencing by: Laboratory for Genomics and Bioinformatics,
University of Genory;
Clone distribution: MGC clone distribution information can be http://inage.lihi.gov
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1 (bases 1 to 938)
S NIH-MGC http://mgc.nci.nih.gov/.
S NIH-MGC http://mgc.nci.nih.gov/.
Interpolate (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapba: r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin information can be found through the I.M.A.G.E. Consortium/LINL at:
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
High quality sequence stop: 767.
High quality sequence stop: 767.
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/note="Organ: ovary; Vector: pOTB7; Site_1: EcoR1; Site_2: Xhoi; cDNA made by oligo-dT priming. Directionally cloned into EcoR1/Xhoi sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagne) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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Bukaryota, Metazoa; Chordate; Craniata; Vertebrata; Euteleostomi;

Bukaryota, Metazoa; Chordate; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;

Hominidae, Homo.

I (bases 1 to 942)

S NIH-McG thtp://mgc.nci.nih.gov/.

I (bases 1 to 942)

L (bases 1 to 942)

L (bupulished (1999)

Contact: Robert Strausberg, Ph.D.

Emal: cgapbe-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

Contact: Preparation: Michael J. Brownstein (NHGRI), Shiraki

Contaction better Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Clone distribution: MGC clone distribution information can be http://image.llnl.gov

Plate: LLAMI1762 row: a column: 11

High quality sequence stop: 762.
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BI600906 IG:15493845
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                          AGGGCGCTGATGGACGAGGAGCCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAAAA
                                                                                                                                                                                    GluvalGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis
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ArgalaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu
                                                                                                                                          CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGGTGCAGGCGGCG
                                                                                            GinLeuThrProvalAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254 AlaGluAlaPheGlnAlaArgLeuLysSerTrpPheGluProLeuValGluAspMetGln
rLysGlu--LeuginAlaAlaGlnAlaArgLeuGlyAlaAspMetGluAspValCysGly
                                                                                                                                                                                                                   713 CAAGGACGCTTGCAGGCGCGCGCAGGCCCGGCTGGGCGGGGACATGGAGGACGTGTGCGGC
                                                                                                                                                                                                                                                                                    114 ArgLeuValGlnTyrArgGlyGluValGlnAlaMetLeuGlyGlnSerThrGluGluLeu
                                                                                                                                                                                                                                                                                                                  134 ArgValArgLeuAlaSerHisLeuArgLysLeuArgLysArgLeuLeuArgAspAlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AspLeuGlnLysArgLeuAlaValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGly
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                                                                                 ysSerGluLeuGlu-GluGln-LeuThrProValAlaGluGluThrArgAlaArgLeuSe
                                                                                                                            AATCGGAACTGGAGGGAACAACCTGACCCCGGTGGCGGAGGAAACGCGGGCACGGCTGTC
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1 (bases 1 to 800)

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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603616028T1 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:5420598 3',
mRNA sequence.
                                                        239
                                                                                                         845
        785
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Contact: More Torp/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1875 row: h column: 07

High quality sequence start: 23

High quality sequence stop: 834.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                220 luMetGlySerArgThrArgAspArgLeuAsp-GluValLys-GluGlnValAlaGluVa
                                                                                                                                                                                          1-ArgAlaLysLeuGluGluGlnAla---GlnGlnIleArgLeuGlnAlaGluAlaPheG
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Indels:
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Homo sapiens
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56 ValThrGlnGluLeuArgAlaLeuMetAspGluThrMet--LysGluLeuLysAlaTyrL 75

8

193

414 213 354

233

234 273

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/organism="Homo sapiens"

/mol_type="mRNA"

/mol_type="mRNA"

/done="Laxon:9606"

/clone="LMAGE:4645759"

/tissue_type="retinoblastoma"

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/tissue_type="retinoblastoma"

/clone lib="NHH MGC 16"

/clone lib="Steel"

/clone lib="NHH MGC 16"

/clone lib="Steel"

/clone lib="NHH MGC 16"

/clone lib="NHH MGC Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit

/cliferinia, Berkeley) using ZAP-CDNA synthesis kit

/cliferinia is a NHH_MGC Library."
                                                                                                                                                                                                          927 bp mRNA linear EST 21-MAR-2001 602513830F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:4645759 5', BG472299
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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644 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGGCCAGCACTGTGGGCTCCCTGGCCGGC
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                                      GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae, Homo.

1 (bases 1 to 927)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
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257
257
113
                                                                                                                  MetGlySerArgThrArgAspArgLeuAspGluVal 232
                                                                                                                                                         763 Ariedecacecedeacececaacecrecacere 798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    164 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu
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  DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.com.i column: 03
Plate: LLCM1875 row: i column: 03
High quality sequence stop: 792.
Location/Qualifiers
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  can
Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://mage.llnl.gov
Plate: LLAM11760 row: b column: 04
High quality sequence stop: 782.
                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                       1. 922
/organism="Homo sapiens"
/mol type="mtNN"
/db_xref="taxon:9606"
/clone="IMAGE:5300259"
/tissue_type="hypothalamus"
/lab_hoste="DH108"
                                                                                                                                                           /clone lib="NIH MGC 96"
/note="Organ: brain; Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-827-854A-2 (1-299) x BI597743 (1-922)
                                                                                                                                                                                                                                                                                       NIH MGC Library."
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BIS97743. GI:15490682
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1 (bases 1 to 922)

1 (bases 1 to 922)

Nath-MOC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CONA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
                                                                                                          CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCCAGCTCCCAGGTCACCCAGGAACTG
                                                                          ValTyrGln-AlaGlyAlaArgGluGlyAlaGluArgGly--LeuSerAlaIleArgGlu
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            GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu
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DEFINITION
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AUTHORS
TITLE
JOURNAL
COMMENT
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BF967543 954 bp mRNA linear EST 23-JAN-2001 602287404T1 NIH_MGC_96 Homo sapiens CDNA clone IMAGE:4374576 3', BF967543
AATGCCGCAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina Poveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Bye Institute (NEI)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lyGluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerH 140
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/dev stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone llb="UT-E-E30"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR 1; Site 2: Not 1;
UT-E-E30 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonolectide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes,
AGAATCAAGA; lens, CGATTAGCGA; eye anterior segment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Soares, MB
Contact: Soares, MB
Contact: Soares, MB
Condinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 9256
Fax: 319 335 9256
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com)
Seq primer: All Revenue.
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                                                                                                         785
                                                                  ydin-ProLeugingluArg-AlaginAlaTrpGlyGluArgLeuArgAlaArgMetGlu 219
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. 706
/organism="Homo sapiens"
/organism="Homo sapiens"
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/clone="UT-E-EJO-aiu-1-08-0-UI"
/tissue_type="fetal eyes, lens, eye anterior segment, optic nerve, retina, Retina Foveal and Macular, RPE and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                 240 ArgAlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGln 258
                                                                                                                                                                                                                                                        846 GGGCCACAAGCTGAAGAAAAAACACCCAGAAATACGCCTTA---GCCGAAGGCTTCAGG 899
  CTGGGGCCCCTGGTGGGAACAGGGCCGGGTGCCGGCCGCCCCTGTGGGCTCCCTGGCCGG
                                                                                          GluMetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 706)

Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate
                                                                                                                                                                                                                                                                                                                                                    BM728696 106 bp mRNA linear EST 01
UI-E-EJO-aiu-1-08-0-UI.rl UI-E-EJO Homo sapiens CDNA clone
UI-E-EJO-aiu-1-08-0-UI 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        BM728696.1 GI:19050022
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Homo sapiens
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E 1 (Dases L t. Co 324)

National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
CDNA Library Preparation: Michael J. Brownstein (LLNL)
DNA Sequencing Dy: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LiNL at:
http://image.lln.gov.
Plate: LLAM1038 row: h column: 01
High quality sequence start: 16
High quality sequence stop: 839.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     644
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 954)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 luThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu-GlnLeuThrProVal
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Matches:
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/organism="Homo sapiens"
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Query Match:
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                                                                                                                 ValGluGluGlyArgValArgAlaAlaThrValGlySerLeuAlaGlyGlnProLeuGln
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                                                                                                                                                                    344 ACCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGCGCCAAGCTGGAG
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CGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCAGGTATCAGGGCC
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2491, Ap 6, Appli

Scoring table:

Searched:

Title: Perfect score:

Sequence:

OM protein

Run on:

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Sequence 1007, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
APPLICANT: OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STRRET: 3174 PORTER DRIVE
CITY: PALO ALTO
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
US-09-949-016-16725
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US-09-818-875-3465
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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-Q-Abss/ABSSWBs spool/10098273854/runat_14062006_081830_26810/app_query.fasta_1

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-LOOPEXT=0 -UNITS=Dits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi

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Sequence 246, App
Sequence 1, Appli
Sequence 2244, Ap
Sequence 3, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
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/EMC Celerra SIDS3/ptodata/2/ina/5_COMB.seq:*
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                                                                                                                     June 14, 2006, 19:03:31 ; Search time 312.205 Seconds
    GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-09-919-039-246
US-07-709-949-1
US-09-108-0107-2244
US-09-108-015-5
US-08-949-155-5
US-09-119-594-155-5
US-01-211-689-37
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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Database :

Score

Result No. 1484 1363.5 1082 1082 1026

3400, Ap 3401, Ap 3404, Ap 3405, Ap 115, App

1386, ĀĒ

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APPLICANT: Kaser, Matthew R.

TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES FILE REPERENCE: PA-0035 US CURRENT APPLICATION NUMBER: US/09/919,039

CURRENT APPLICATION NUMBER: US/09/919,039

PRIOR PILLING DATE: 2002-09-09

PRIOR PILLING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 401

SOFTWARE: PERL Program

SEQ ID NO 246

LENGTH: 1291
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OTHER INFORMATION: Incyte ID No. 6727066 2514988CB1
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ORGANISM: Homo sapiens
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COTHER INFORMATION:
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NAME/KEY: unsure
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERNE/COKET NUMBER: 37,071
REFERNE/COKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1007:
SEQUENCE CHARACTERISTICS:
LENGTH: 1156 base pairs
TYPE: Nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: GENERAL
CLONE: 9178850
US-09-023-655-1007
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Best Local Similarity:
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Pred. No.:
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Journal of Biological Chemistry
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1484.00
99.3%
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                                                    LENGTH: 1157 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRN
                                                                                                                                                                                                               ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc signal
LOCATION: 62.119
PUBLICATION INFORMATION:
AUTHORS: McLean, J W
JOURNAL: 259
                              SEQUENCE CHARACTERISTICS
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LOCATION:
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                                                    GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis
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                                                                                           600 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGGTGCGCCTCGCCTCCCAC
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPOTER: IBM PC COMPAILS
COMPOTER: IBM PC COMPAILS
COMPAGE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/709,949
FLING DATE: 19910604
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 9629691801
TELECHMONICATION INFORMATION:
TELECHMONICATION 18000
TELEFRAX: (608) 251-5000
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Patent No. 5472858
GENERAL INFORMATION:
APPLICANT: Attie, Alan D
APPLICANT: Gretch, Daniel G
APPLICANT: Sturley, Stephen L
APPLICANT: Beckage, Nancy E
TITLE OF INVENTION: Production of Rec;
TITLE OF INVENTION: Insect Larvae
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Quarles & Brady
STREET: P.O. Box 2113
CITY: Madison
STATE: WI
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Patent No. 6524613
GENERAL INFORMATION:
APPLICANT: Steer, Clifford J.
Kren, Betsy T.
Bandyopadhyay, Paramita
ROY-Ghowdhury, Jayanta
TITLE OF INVENTION: Hepatocellular Chimeraplasty
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
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APPLICATION NUMBER: US/09/108,006C
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                                                CTGGGGCCCCTGGTGGAACAGGGCGCGTGCGGGCCGCCACTGTGGGGCTCCCTGGCCGC
                                                                                                         GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu
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          LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly
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Matches:
Conservative:
Mismatches:
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Sequence 2244, Application US/09880107

Batent No. 6974667

GENERAL INFORMATION:

APPLICANT: Horne, Darci T.

APPLICANT: Vockley, Joseph G.

APPLICANT: Gene Logic, Inc.

ITILE OF INVENTION: Gene Expression Profiles in FILE OF PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950

SOFTWARE: Patentin Ver. 2.1

LENGTH: 1157
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArgLeuLysSerTrpPheGlu
                                                                                                                                                                                                                                                          AspMetGluAspValCysGlyArgLeuValGlnTyrArgGlyGluValGlnAlaMetLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147 ArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAlaValTyrGlnAlaGlyAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2221 GAGGTGAGTGTCCCCATCCTGGCCCTTGACCCTCCTGGTGGGCGGCGCTATACCTCCCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 GinSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3805
298
0
1
195
1
FILING DATE: 30-Jun-1992
CLASSIFCATION: «Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,837
APPLICATION NUMBER: 60/064,937
FILING DATE: 05-AUG-1997
APPLICATION NUMBER: 60/064,996
FILING DATE: 10-NOV-1997
APPLICATION NUMBER: 60/074,497
FILING DATE: 12-FEB-1998
APPLICATION NUMBER: 60/074,497
FILING DATE: 12-FEB-1998
APPLICATION NUMBER: 90/0834
FILING DATE: 30-APR-1998
ATTORNEY/AGRNT INFORMATION:
NAME: Friebel, Thomas
REGISTRATION NUMBER: 2926
TELECOMMUNICATION INFORMATION:
TELEFRANCE/DOCKET NUMBER: 7991-015-999
TELEFRANCE/DOCKET NUMBER: 7991-015-999
TELEFRANCE/DOCKET NUMBER: 7991-015-999
TELEFRANCE/DOCKET NUMBER: 7991-015-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: exon
LOCATION: 71...114
OTHER INFORMATION: Exon 1
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                               TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3805 base pairs
                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.27e-122
1363.50
60.4%
60.4%
91.3%
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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                                ProvalAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAlaGlnAlaArg 103
                                                                                                     104 LeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGlyGluValGln 123
                                                                                                                                    411 Gregececedecarecarectecarecectregreerectrececeaeceaeceaece 470
                                                                                                                                                                                            164 AlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArgLeuGlyPro 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 GlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGluMetGlySer 223
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                                                                                                                                                                                                                                          LeuargiysargleuleuargaspalaaspaspheuGlniysargleualayalTyrGln
                                                          124 AlametLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHisLeuArgLys
                                                                                                                                                                                                                                                                                                                                   Bazer, Fuller W
TITLE OF INVENTION: Compositions and Methods for the
Generation of Transgenic Animal Species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             284 GlnAlaAlaValGly---ThrSerAlaAlaProValProSerAspAsn 298
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE AND DURKEE
STREET: P.O. BOX 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/819,964
FILING DATE: 28-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Piedrahita, Jorge A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09819964; Patent No. 6369294; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Houston
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APPLICANT: Bazer, Fuller W
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Generation of Transgenic Animal Species
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSE: ARNOLD, WHITE AND DURKEE
STREET: P.O. Box 4433
CITY: Houston
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212
40
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2
                                                                                                                                                                                                                                                                                                             MEDIUM TIPE: Flogy disk.

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SUSTWARE: Batentin Release #1.0, Version #1.30

SURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/949,155

FILING DATE: CONCURRENTLY Herewith

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/027,338

FILING DATE: 11-0CT-1996

PRIOR APPLICATION NUMBER: US 60/046,094

FILING DATE: 09-MAY-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REFERENCE/DOCKET NUMBER: TAMK:177

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFRAX: (713) 789-2679

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERITICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
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                     Sequence 5, Application US/08949155 Patent No. 6271436
                                                                                                                                                                                                           CITY: Houston
STATE: TX
COUNTRY: US
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDLUM TYPE: FLORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.04e-95
1082.00
85.1%
71.6%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51..1001
                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , LOCATION:
US-08-949-155-5
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       US-08-949-155-5
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DB:
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APPLICANT: Zhong, Mei
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHC
FILE REFERENCE: 21402-4168
FILE REFERENCE: 21402-4168
CURRENT PILLING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: 60/311751
PRIOR APPLICATION NUMBER: 60/311751
PRIOR APPLICATION NUMBER: 60/3110, 802
PRIOR PLING DATE: 2001-08-08
PRIOR PLING DATE: 2001-08-08
PRIOR PLING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/311, 292
PRIOR PLING DATE: 2001-08-09
PRIOR PLING DATE: 2002-04-16
PRIOR PLING DATE: 2002-04-16
PRIOR PLING DATE: 2002-04-16
PRIOR PLING DATE: 2002-05-15
PRIOR PLING DATE: 2002-05-15
PRIOR PLING DATE: 2001-08-13
PRIOR PLING DATE: 2001-08-13
PRIOR PLING DATE: 2001-08-13
PRIOR PLING DATE: 2001-08-13
PRIOR PLING DATE: 2001-08-14
PRIOR PLING DATE: 2001-08-15
PRIOR PLING DATE: 2001-08-13
PRIOR PLING DATE: 2001-08-13
PRIOR PLING DATE: 2001-08-14
PRIOR PLING DATE: 2001-08-16
PRIOR PLING DATE: 2001-08-16
PRIOR PLING DATE: 2001-08-13
                                                                                                                                                             GluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArgLeuLysSer 263
                                                                                                                                                                                                                                                                   891 TGGTTCGAGCCTCTGGTGGAAGACATACGGCGCCAGTGGGCCCGGGCTGGTGGAGAGATG 950
                                                                                                      771 CGGACCCGCGACCGCCTGGATGAGATGCGTGAGCAGCTGGAGGAGGAGGAGGGCGCACCAAAGTG
                       ArgThrArgAspArgLeuAspGluValLysGluGluValAlaGluValArgAlaLysLeu
                                                                                                                                                                                  TrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuValGluLysVal
  GlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGluMetGlySer
                                                                                                                                                                                                                                                                                                                                                                   966
                                                                                                                                                                                                                                                                                                                          284 GlnAlaAlaValGly---ThrSerAlaAlaProValProSerAspAsn 298
                                                                                                                                                                                                                                                                                                                                                    Sequence 37, Application US/10211689 Patent No. 6974684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INPORMATION:
APPLICANT: Algebrook, John II
APPLICANT: Anderson, David W.
APPLICANT: Boldog, Ferenc L.
APPLICANT: Garman, Stacie J.
APPLICANT: Garman, Stacie J.
APPLICANT: Garman, Stacie J.
APPLICANT: Gorman, Linda
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Smithson, Glennda
Spytek, Kimberly A.
Vernet, Corine A. M.
Voss, Edward Z.
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MacDougall, John R.
Pena, Carol A.
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Patturajan, Meera
Rieger, Daniel K.
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US-10-211-689-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGGTGGAGCCGGTTGGCGCCGCCCACACAGAGCCGGCCAGCCGCTG 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAlaGlnAlaArg 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuGlyalaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGlyGluValGln 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 AlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHisLeuArgLyB
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-827-854A-2 (1-299) x US-09-819-964-5 (1-1126)
            FILING DATE: AUGMENTS
APPLICATION NUMBER: US 60/046,094
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
FELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-1000
TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: 08/949,155
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: US-09-819-964-5
                                                                                                                                                                                                                                                        LENGTH: 1126 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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1082.00
85.1%
71.6%
                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
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Best Local Similarity:
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US-10-215 (19-35)
US-10-215 (19-35)
US-10-21-15 (19-35)
US-10-21-1
                                                                            GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGCCGGGCTGGTG
                                                                                                         599 GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCCCCTGTGCCCAGCGACAATCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             718
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US-10-211-689-35
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Pred. No.:
Score:
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LENGTH: 718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTTGGGATTACCTGCGCTGGGTG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 CAGACACTGTCTGAGCAGGAGGAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGCAGAGTGG
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                                                                                                                                                                                                                                                                                      664
214
10
14
84
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                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
          SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 37
LENGTH: 664
                                                                                                                                                                                                                                                                                   2.628-90
1026.00
71.6%
71.6%
68.7%
                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                          ) NAME/KEY: CDS
; LOCATION: (2)..(664)
US-10-211-689-37
                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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TYPE: DNA
ORGANISM: Homo sapiens
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US-10-211-689-31
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Best Local Similarity:
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                                                            APPLICANT
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                                                                                                                                                         CAGACACTGTCTGAGCAGGTGCAGGAGCTGCTCAGCTCCCAGGTCACCAGGAACTG 244
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          0 1 8 1 0
          Conservative:
Mismatches:
Indels:
Gaps:
                                                                           US-09-827-854A-2 (1-299) x US-10-211-689-35 (1-718)
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Patent No. 6974684
GENERAL INFORMATION:
APPLICANT: Alsobrook, John II
          71.6$
71.6$
68.7$
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-10-211-689-31
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APPLICANT: Balday Catherine E.
APPLICANT: Gaman, Indiana, A.
APPLICANT: Maccadal, John R.
APPLICANT: Patcherial, Mera R.
APP
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APPLICANT: Shinkets, Nainet.
APPLICANT: Shinkets, Richard A.
APPLICANT: Shinkets, Richard A.
APPLICANT: Shinkets, Richard A.
APPLICANT: Shinkets, Richard A.
APPLICANT: Shinkets, Rimberly A.
APPLICANT: Shinkets A.
APPLICANT: Vernet, Corine A. M.
APPLICANT: Loss, Edward 2.
APPLICANT: Zhong, Mei
TITLE OF INVERTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHON FILE REPERENCE: 2010-10-12
FURRENT APPLICATION NUMBER: 06/310,802
PRIOR FILING DATE: 2001-08-08
PRIOR FILING DATE: 2001-08-08
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2002-02-28
PRIOR FILING DATE: 2002-02-28
PRIOR FILING DATE: 2002-02-28
PRIOR FILING DATE: 2002-02-28
PRIOR FILING DATE: 2002-02-38
PRIOR FILING DATE: 2002-02-38
PRIOR FILING DATE: 2002-03-39
PRIOR FILING DATE: 2002-04-16
PRIOR FILING DATE: 2002-04-16
PRIOR FILING DATE: 2002-04-16
PRIOR FILING DATE: 2002-04-16
PRIOR FILING DATE: 2002-06-16
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-14
PRIOR FILING DATE: 2001-06-14
PRIOR FILING DATE: 2001-06-15
PRIOR FILI
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Patturajan, Meera
Rieger, Danial K.
Shimkets, Richard A.
Smithson, Glennda
Spytek, Kimberly A.
Vernet, Corine A. M.
Voss, Edward Z.
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Best Local Similarity:
Query Match:
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132 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG 191
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Patent No. 6974684
GENERAL INFORMATION:
APPLICANT: Alsobrook, John II
APPLICANT: Boldog, Ferenc. L.
APPLICANT: Boldog, Ferenc. L.
APPLICANT: Burgess, Catherine B.
APPLICANT: Gaman, Stacie J.
APPLICANT: Gaman, Stacie J.
APPLICANT: Gangolli, Esha A.
APPLICANT: Gorman, Linda
APPLICANT: Gorman, Linda
APPLICANT: Gorman, Linda
APPLICANT: Lepley, Denise M.
APPLICANT: Lepley, Denise M.
APPLICANT: Lepley, Denise M.
APPLICANT: Peyman, John R.
APPLICANT: Peyman, John A.
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PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/310,802
PRIOR APPLICATION NUMBER: 60/310,795
PRIOR FILING DATE: 2001-08-08
PRIOR PILING DATE: 2001-08-08
PRIOR PELING DATE: 2001-08-09
PRIOR PELING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/361,159
PRIOR APPLICATION NUMBER: 60/361,159
PRIOR APPLICATION NUMBER: 60/373,050
PRIOR PILING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: 60/380,970
PRIOR PILING DATE: 2002-05-15
PRIOR PELING DATE: 2001-08-13
PRIOR PELING DATE: 2001-08-13
PRIOR PELING DATE: 2001-08-13
PRIOR PILING DATE: 2002-05-16
PRIOR PILING DATE: 2002-05-16
PRIOR PILING DATE: 2001-09-21
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US-10-211-689-41
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CURRENT APPLICATION NUMBER: US/10/211,689
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: 60/311751
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Patent No. 6974684
GENERAL INFORMATION:
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APPLICANT: Anderson, David W.
APPLICANT: Boldog, Ferenc L.
APPLICANT: Boldog, Ferenc L.
APPLICANT: Casman, Stacie J.
APPLICANT: Casman, Stacie J.
APPLICANT: Gangolli, Esha A.
APPLICANT: Gorman, Linda
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Lepley, Denise M.
APPLICANT: Lepley, Denise M.
APPLICANT: Peyman, John R.
APPLICANT: Peyman, John R.
APPLICANT: Peyman, John A.
APPLICANT: Shimkets, Richard A.
APPLICANT: Schimberly A.
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Patturajan, Meera
Rieger, Daniel K.
Shimkets, Richard A.
Smithson, Glennda
Spytek, Kimberly A.
Vernet, Corine A. M.
Voss, Edward Z.
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PRIOR APPLICATION NUMBER: 60/311,979
PRIOR FILING DATE: 2001-08-13
PRIOR PILING DATE: 2004-08-13
PRIOR PLING DATE: 2004-05-16
PRIOR PILING DATE: 2004-05-16
PRIOR FILING DATE: 2004-09-21
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 132
SOFTWARE: CURASeqList version 0.1
LENGTH: 788
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ORGANISM: Homo sapiens
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; LOCATION: (18)..(704)
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APPLICANT: Alabornow, John II.
APPLICANT: Burgess, Catherine E.
APPLICANT: Ganguli, Esha A.
APPLICANT: Ganguli, Esha A.
APPLICANT: Ganguli, Esha A.
APPLICANT: Alabornow, Nikolai V.
APPLICANT: APPLICANT: Alabornow, Nikolai V.
APPLICANT: Perman, Obnn R.
APPLICANT: Perman, Obnn R.
APPLICANT: Rieger, Dohn R.
APPLICANT: Rieger, Dohn R.
APPLICANT: Rieger, Dohn R.
APPLICANT: Smithson, Glanda
APPLICANT: Smithson, Glanda
APPLICANT: Smithson, Glanda A.
APPLICANT: Smithson, Glanda
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        161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
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                                                                                                                                                              201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu
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Patent No. 6974684
GENERAL INFORMATION:
APPLICANT: Alachrook, John II
APPLICANT: Boldog, Perenc L.
APPLICANT: Burgess, Catherine E.
APPLICANT: Gasman, Stacie J.
APPLICANT: Gasman, Stacie J.
APPLICANT: Gargolli, Esha A.
APPLICANT: Gargolli, Esha A.
APPLICANT: Gargolli, Esha A.
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                                                GlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpValGlnThrLeu
                                                                                                             SerGluGlnValGluGluLeuLeuSerSerGlnValThrGlnGluLeu-----
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                                                                                                           LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal
                                              241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg
                                                                             -----CTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTTCCAGGCCCGC
                                                                                                                                                                                                                                                                                                                      APPLICANT: Piedrahita, Jorge A
APPLICANT: Bazer, Fuller W
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Generation of Transgenic Animal Species
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4267
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APPLICATION NUMBER: US/08/949,155 FILING DATE: CONCURRENTLY Herewith CLASSIFICATION: 800 PRIOR APPLICATION NUMBER: US 60/027,338 FILING DATE: 11-OCT-1996 PRIOR APPLICATION NUMBER: US 60/046,094 FILING DATE: 09-MAY-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                       Sequence 51, Application US/08949155
Patent No. 6271436
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Houston
STATE: TX
COUNTRY: US
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 51:
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TYPE: nucleic acid
STRANDEDNESS: single
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Pred. No.:
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2490 GAGCCGGGCGCCGCCGGAGGTGCACGTGTGGTGGGAGGAGGCCCAAGTGGCAGGGCAGG
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                                                    24 GlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpValGlnThrLeu
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         GTGCGCACCAAAGTGGAGGAGCAGGCAGCCAGTTGCGCCTGCAGGCCGAGGGATTCCAC
                                                                                  LeuvalGluLysValGlnAlaAlaValGly --- ThrSerAlaAlaProValProSerAsp
                                                      AlaArgLeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGly
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Transgenic Animal Species
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/949,155
FILING DATE: «Unknown»
APPLICATION NUMBER: US 60/046,094
FILING DATE: 09-MAY-1997
ATTORNEY/AGBHT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 14,071
REFERENCE/DOCKET NUMBER: TAMK:177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE AND DURKEE
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/819,964
FILING DATE: 28-Mar-2001
CLASSIFICATION: CURKNOWN>
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                        Sequence 51, Application US/09819964
Patent No. 6369294
GENERAL INFORMATION:
APPLICANT: Piedrahita, Jorge A
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STRANDEDNESS: single
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SEQUENCE CHARACTERISTICS:
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ZIP: 77210-4433
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Best Local Similarity:
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Sequence 655, App
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Sequence 3, Appli
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Sequence 1, Appli
Sequence 17, Appl
Sequence 1, Appli
Sequence 1007, Ap
Sequence 125, App
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Sequence 1291, Ap
Sequence 4536, Ap
Sequence 3, Appli
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Sequence 3, Appli
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Sequence 106,
Sequence 63,
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Sequence 1, Ap
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Sequence 63, Application US/10257021
Sequence 63, Application US/10257021
Sequence 63, Application No. US20030211498A1
GENERAL INFORMATION:
APPLICANT: Sherman-Baust,
APPLICANT: Sherman-Baust,
APPLICANT: Hough, Colleen D.
TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER FILE REFERENCE: 14014.0369U2
CURRENT FILING DATE: 2002-10-03
PRIOR FILING DATE: 2001-04-03
PRIOR FILING DATE: 2001-04-03
PRIOR FILING DATE: 2001-04-03
PRIOR FILING DATE: 2000-04-03
PRIOR FILING DATE: 2000-04-03
SOFTWARE: FASE IN NUMBER: 60/194,336
NUMBER OF SEQ ID NOS: 147
                                                                                                                                                         US-10-852-335A-10
US-10-937-758A-106
US-10-773-446-63
US-11-186-284-5
US-11-055-309A-1
US-10-929-182-34
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US-11-055-309A-3
         US-09-870-759-129
US-09-802-640-17
US-09-751-708A-129
US-10-301-822-5
US-10-403-902A-17
US-10-441-641-641
US-10-428-851-1
US-10-641-643-1007
US-10-794-125
US-10-794-125
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US-10-044-090-454
US-10-10-10-68-08-38
US-09-827-854-12
US-09-827-854-19
US-09-827-854-11
US-09-827-854-11
US-09-827-854-11
US-09-827-854-11
US-09-80-107-2244
US-09-960-106-655
US-09-960-106-655
US-09-960-106-655
US-10-313-641-3
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                            Published Applications NA Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10P_PUBCOMB.seq:*
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16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*
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-Q=/abss/ABSSWEB spool/US09827854/runat_14062006_081838_26978/app_query.fasta_1
-Q=/abss/ABSSWEB spool/US09827854/runat_14062006_081838_26978/app_query.fasta_1
-DB=Published Applications NA Main -QFWT=fastap -SUFFIX=p2n.rnpbm
-MINWATCH=0.1_LOOPCL=0 -LÕOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE-LOCAL -OUTFWT=pto -NORM=ext
-HRAFSIZE=500 -MINILEN=0 -ALIGN=15 -MODE-LOCAL -OUTFWT=pto -NORM=ext
-USR=US09827854_@CGN 1_1_2326_@runat_H062006_081838_26978 -NCPU=6 -ICPU=3
-NO WMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-NARN_TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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             GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                      - nucleic search, using frame_plus_p2n model
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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Maximum DB seq length: 2000000000
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1493
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Match Length DB
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Database :

Result

Sequence 3787, Ap

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Sequence 126, App Sequence 3, Appli

256, App 8338, Ap 12, Appl 9, Appli

Sequence Sequence Sequence

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9.78e-135
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                                                                                                                                       TYPE: DNA
CORGANISM: Homo sapiens
US-09-827-854-8
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Query Match:
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Sequence 8, Application US/09827854
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GENERAL INFORMATION:
APPLICANT: Zannis, Vassilis
APPLICANT: Zannis, Vassilis
APPLICANT: Zannis, Vassilis
APPLICANT: Zannis, Vassilis
TITLE OF INVENTION: Compounds and methods for lowering
TITLE OF INVENTION: Cholesterol levels without inducing hypertriglyceridemia
FILE REPRENENCE: 07180/00403
CURRENT APPLICATION NUMBER: US/09/827,854
CURRENT APPLICATION NUMBER: US/09/827,865
PRIOR APPLICATION NUMBER: US/09/59,088
PRIOR PLING DATE: 2000-10-04
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 1156 140 160 180 200 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100 414 120 474 594 654 714 174 354 234 294 40 9 80 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly cadececederadececedanadadeacenenarecececececearecadanaceece gagerecageccarecreeccagadeacceagagereceegreececreecac LeudrgLysLeudrgLysArgLeuLeudrgAspAladspAspLeuGlnLysArgLeudla CTGCGCAAGCTGCGTAAGCGGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly CTGGGGCCCCTGGTGGAACAGGGCCGCGTGGGGCGGCCCACTGTGGGCTCCCTGGCCGGC CAGACACTICTICTICAGCAGCAGCAGCAGCAGCTGCTCCAGCTCCCAGGTCACCCCAGGAACTG LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 1156 299 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: US-09-827-854A-2 (1-299) x US-09-827-854-8 (1-1156)

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CAGGCCCGGCTGGGCCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC
                                       GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis
                                                      GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGGGGCGCCTCGCCTCCCAC
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OTHER INFORMATION: Nucleotide Sequence encoding apolipoprotein
OTHER INFORMATION: (APOE)
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| Sequence 17, Application US/09802640
| Publication No. US20030036057A1
| GENERAL INFORMATION:
| APPLICANT: Braun, Andreas
| APPLICANT: Kleyn Patrick;
| TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
| TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE
| FILE REPERENCE: 24736-2048
| CURRENT FILING DATE: 2001-03-09
| WUMBER OF SEQ ID NOS: 122
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 17
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ORGANISM: Homo sapien
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 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCCGGCTGGTG 954
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US-09-870-759-129
Sequence 129, Application US/09870759
Fetent No. US20020177551A1
GENERAL INFORMATION:
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
FILE REFERENCE: 870759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT APPLICATION NUMBER: US 60/208,128
FRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SEQ ID NO 129
LENGTH: 1156
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LOCATION: (61)..(1014)
OTHER INFORMATION:
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                9.78e-135
1493.00
100.0%
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PRIOR FILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 166
SOFTWARE: PatentIn version 3.1
SEQ ID NO 129
                                                                                                        ; LOCATION: (61)..(1014)
; OTHER INFORMATION:
US-09-751-708A-129
                                                              TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                  NAME/KEY: CDS
                                                                                                                                                            Alignment Scores:
Pred. No.:
                                                  LENGTH: 1156
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Sequence 129, Application US/09751708A
Sequence 129, Application US/09751708A
Dublication NO. US20030157113A1
GENERAL INFORMATION:
APPLICANT TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 751708
CURRENT PELLING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 60/173,371
                                                                                                                                                                                                                                                                                                                      GluvalGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
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                                           CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA
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                          LysvalGluGlnAlavalGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp
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Sequence 1, Application US/10313641

Sequence 1, Application US/10313641

Bublication No. US20030162758A1

GENERAL INFORMATION:

APPLICANT: Ishida, Brian

APPLICANT: Bailey, Kathy

APPLICANT: Bailey, Kathy

APPLICANT: Schwartz, Daniel

TITLE OF INVENTION: Treatments for Age Related-Macular Degeneration (AMD)

FILE REPERIOR: 2002-10-06

CURRENT APPLICATION NUMBER: US 60/415,864

PRIOR PELLING DATE: 2002-10-03

PRIOR APPLICATION NUMBER: US 60/415,864

PRIOR PELLING DATE: 2001-12-07

PRIOR APPLICATION NUMBER: US 60/340,498

PRIOR SEQ ID NOS: 12

SOFTWARE: Patentin version 3.1

TEMPORE APPLICATION NUMBER: US 60/340,498
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CAACTGACCCCGGTGGGGGGGGGGGCGCGCCCCTCCCAAGGAGGCTGCGGGCGCG
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                                                                                                  415 CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC
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ORGANISM: Human
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APPLICANT: Berger, Allison
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Guillemette, Tracy L.
APPLICANT: Guillemette, Tracy L.
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Murgart, Lawrence N.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, THERAPY OF COLON CANCER
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, MURBER: US 60/391,971
FILE REPREDENCE: MPMO1-029P2RNM
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/381,978
PRIOR PLING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SUPPRARE: PASTSEC for Windows Version 4.0
                                           LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
                                                                 895 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCCAGTGGGCCGGGCTGGTG 954
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                                                                                                                                                                                                                                     Sequence 5, Application US/10301822 Publication No. US20030148410A1 GENERAL INFORMATION:
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ORGANISM: Homo Sapiens
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Best Local Similarity:
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OTHER INFORMATION: Nucleotide Sequence encoding apolipoprotein
OTHER INFORMATION: (APOE)
TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE FILE REPERBNCE: 2473-2048 CURRENT APPLICATION NUMBER: US/10/403,902A CURRENT FILING DATE: 2003-07-21 PRIOR APPLICATION NUMBER: 09/802,640 PRIOR APPLICATION NUMBER: 09/802,640 PRIOR PILING DATE: 2001-03-09 SHOW FILING DATE: 2001-03-09 SOFTWARE: FASESEQ for Windows Version 4.0
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ORGANISM: Homo sapien
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                                      GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
CLASSIFICATION: <UNKNOWD>
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Sugan G. Stuart
Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR
GENE EXPRESSION
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APPLICATION NUMBER: «Unknown»
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence 1007, Application US/10641643
; Publication No. US20040077003A1
; GENERL INFORMATION:
APPLICANT: Cocks, Benjamin G.
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ADDRESSEE: INCYTE PHARMACI
STREET: 3174 PORTER DRIVE
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STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
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US-10-641-643-1007
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; Bublication No. US2003022962A1
; Bublication No. US2003022962A1
; GENERAL INFORMATION:
    APPLICANT: Ishida, Brian
; APPLICANT: Bailey, Kathy
; APPLICANT: Bailey, Kathy
; APPLICANT: Bailey, Kathy
; APPLICANT: Bailey, Mathy
; APPLICANT: Bolley, Mathy
; APPLICANT: Schwartz, Daniel
; TITLE OF INVENTION: Treatments for Age Related-Macular Degeneration (AMD)
; FILE REFERENCE: P0231083
; CURRENT APPLICATION NUMBER: US 60/415,864
; PRIOR FILING DATE: 2001-10-03
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1156
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Gaps:
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Best Local Similarity:
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
Pred. No.:
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: TERRAN, David S

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE

FILE REPRENEUE: 38373-189118

CURRENT APPLICATION NUMBER: US 60/378,988

PRIOR APPLICATION NUMBER: US 60/378,988

PRIOR PILING DATE: 2002-05-08

PRIOR PILING DATE: 2002-06-15

PRIOR FILING DATE: 2002-06-15

PRIOR FILING DATE: 2002-06-15

PRIOR FILING DATE: 2002-06-16

PRIOR FILING DATE: 2002-06-16

PRIOR FILING DATE: 2002-06-08

PRIOR FILING DATE: 2002-00-01

PRIOR FILING DATE: 2002-10-01

PRIOR FILING DATE: 2002-10-01

PRIOR FILING DATE: 2002-10-02

PRIOR FILING DATE: 2003-01-09

PRIOR FILING DATE: 2003-01-09

NUMBER OF SEQ ID NOS: 224

SOFTWARE: PATENTIN VEXEION 3.2

SEQ ID NO 125

**MADE: NA
                                   AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
                                                                                                          LeulysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
 775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 834
                                                        1 LysvalGluGlnAlavalGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp
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Matches:
Conservative:
Mismatches:
Indels:
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ORGANISM: Homo sapiens
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US-10-428-817A-125
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Matches:
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REGISTRATION NUMBER: 37,071
REPERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUTCATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1007:
SEQUENCE CHARACTERISTICS:
LENGTH: 1156 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
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                                                                                                                                                                                                                                                           NO: 1007
                                                                                                                                                                                                                                      CLONE: 9178850
SEQUENCE DESCRIPTION: SEQ ID
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                                                     Length:
Matches:
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Mismatches:
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US-10-794-198A-1
  TYPE: DNA ORGANISM: 1
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Sequence 1. Application US/10794198A

Publication No. US20040266663A1

Sequence 1. Application US/10794198A

Publication No. US20040266663A1

Sepuence 1. Application No. US20040266663A1

APPLICANT: Schwartz, Daniel

APPLICANT: Bailey, Kathy

FILE OF INVENTION: ENTHABLE US NO. 10794, 198A

CURRENT FILING DATE: 2004-03-05

PRIOR PLICATION NUMBER: US 10/428,551

PRIOR PLICATION NUMBER: US 60/340,498

PRIOR PLICATION NUMBER: US 60/340,498

PRIOR APPLICATION NUMBER: US 60/340,498

PRIOR APPLICATION NUMBER: US 60/340,498

PRIOR APPLICATION DATE: 2002-12-06

PRIOR APPLICATION NUMBER: US 60/340,498

PRIOR PLING DATE: 2002-110-03

NUMBER OF SEQ ID NOS: 17

SEQ ID NO 1

LENGTH: 1156
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                   GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla
                                    CAACTGACCCCGGTGGCGGAGGAGACGCGGCACGGCTGTCCCAAGGAGCTGCAGGCGCG
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CTHER INFORMATION:

US-10-937-758A-106
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                                            Sequence 10, Application US/10852335A; Publication No. US20050112129A1; Sequence 10, Application No. US20050112129A1; Subjication No. US20050112129A1; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Compositions and Methods for the Diagnosis and TITLE OF INVENTION: Treatment of Tumors of Glial Origin; FILE REPERENCE: E5103R1-US.
CURRENT APPLICATION NUMBER: US 60/548,299; RIOR PELING DATE: 2004-05-24; PRIOR PELICATION NUMBER: US 60/473,238; PRIOR FILING DATE: 2003-05-23; PRIOR FILING DATE: 2003-05-23; NUMBER OF SEQ ID NOS: 190; SEQ
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Best Local Similarity:
Query Match:
DB:
                   RESULT 13
US-10-852-335A-10
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RESULT 14

US-10-937-758A-106

SQUENCE 106, Application US/10937758A

SQUENCE 106, Application US/10937758A

SQUENCE 106, Application NO. US20050112141A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE

CURRENT APPLICATION NUMBER: US/10/937,758A

CURRENT PILING DATE: 2004-09-08

PRIOR APPLICATION NUMBER: 09/650,884

PRIOR APPLICATION NUMBER: 09/650,884

SPRIOR FILING DATE: 2000-08-30

NUMBER OF SEQ ID NOS: 121

SOFTWARE: PARENTIN Version 3.1

SEQ ID NO 106
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GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu
                     MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg
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Conservative:
Mismatches:
Indels:
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LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
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US-10-773-446-63

Sequence 63, Application US/10773446

Sequence 63, Application WO/10773446

Publication No. US20050176662A1

GENERAL INFORMATION:

APPLICANT: INANA, GENERE

TITLE OF INVENTION:

TITLE OF INVENTION:

FILE REPERENCE: 39532-19229

CURRENT APPLICATION NUMBER: US/10/773,446

CURRENT PILING DATE: 2004-02-09

CURRENT PILING DATE: 2004-02-09

NUMBER OF SEQ ID NOS: 131

SOFTWARE: PATENTIN Version 3.2

SEQ ID NO 63

LENGTH: 1156

TYPE: DNA

ORGANISM: Homo sapiens
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115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG
                GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal
                          175 CAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG
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AX409597 Sequence
M12529 Human apoli
X13887 Monkey mRNA
BC003557 Homo sapi
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Patent: US 546593-A 10 14-NOV-1995;
Location/Qualifiers
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10 from patent US 5466593.
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AR075563
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/organism="unknown"
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-MODEL=frame+_p2n.model -DEV=x1h
-MODEL=frame+_p2n.model -DEV=x1h
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-OUTFWIT=pto -NORM=ext -HEAPSIZE=50 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02h
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 I15467 Sequence 10
I69313 Sequence 10
AR211787 Sequence
                                                                                               June 14, 2006, 19:02:13; Search time 557.375 Seconds (without alignments) 3097.698 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
            GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                      - nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Database :

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ASTOOLIO 117 bp DNA linear SYN 08-NOV-1996
Artificial sequence DNA for expression cassette, toolbox 10.
Y09270
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I (bases 1 to 275)

In (bases 1 to 275)

Characterization of different mRNA types expressed in human brain Unpublished

2 (bases 1 to 275)

Dmitrenko, V. V.
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (12-AR-1996) Dmitrenko V. V., Institute of Molecular
Biology and Genetics, Biosynthesis of Nucleic Acids, Zabolotnogo
150, Kiev, Ukraine, 252627
                                                                                                                                                                                                                 Unpublished
2 (bases 1 to 117)
Schluseener, H.J.
Direct Submission
Submitted (21-OCT-1996) H.J. Schluseener, Inst.f. Hirnforschung,
Calwer Str. 3, D- 77076 Tuebingen, FRG
                                                                                                                                                                                                                                                                                                                                                                     1. .117
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         1 ATGAAGGTTCTGTGGGCTTGCTGGTCACATTCCTCGCAGGATGCCAGGCC
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H.sapiens mRNA for apolipoprotein E (partial).
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/mol_type="other DNA"
/db_xref="taxon:32630"
1. .117
                                                                                                                                                                               other sequences; artificial sequences.
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apolipoprotein E.
Homo sapiens (human)
Homo sapiens
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                                                                                                                               PAT 04-FEB-1998
                                                                                                                                                                                                           Unclassified.

1 (bases 1 to 93)
1 (bases 1 to 93)
2 Falduco, M.T., Magnuson, S.R. and Morgan, D.W.
Human matrix metalloprotease gene, proteins encoded therefrom and methods of using same
Patent: US 6399371-A 4 04-UUN-2002;
Location/Qualifiers
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Sequence 10 from patent US 5677164.
169313 GI:2831435
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Sequence 4 from patent US 6399371.
AR211787
AR211787.1 GI:21515202
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                         US-09-827-854A-13 (1-18) x I15467 (1-71)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                               Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y. Expressed sequence tags and encoded human proteins Patent: EP 1033401-A 2137 06-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unknown.
Unclassified.
Unclassified.
(I (bases 1 to 405)
Edwards,J.-B.D.M., Duclert,A. and Giordano,J.-Y.
Expressed sequence tags and encoded human proteins
Patent: US 6783961-A 2137 31-AUG-2004;
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Sequence 2137 from Patent EP1033401.
AX886274
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Gaps:
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/organism="unknown"
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38. .>275
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G06F15/40
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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                                                                         /mol_type="minorage: color: blue;" | mol_type="minorage: color: blue;" | mol_type="minorage: color: blue;" | mol_type="minorage: color: blue;" | fulsione type="brain" | fulsione type="brain" | fulsione type="brain" | fulsione type="fetus" | fulsione type="fetus" | fulsione type="fetus" | fulsione type="molipoprotein E" | fulsione to K00396" | fulsione to K00396" | fulsione type="molipoprotein E" | fulsione type="molipoprotein E" | fulsione type="fetus" | ful
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Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
Sequence tag and encoded human protein
Patent: JP 2001269182-A 2130 02-OCT-2001;
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119. .403.
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JP 2001269182-A/2130
02-0CT-2001
24-FEB-2000 JP 2000118773
26-FEB-1999 US 60/122487

    .405
    /organism="Homo sapiens"

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ocation/Qualifiers
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JP 2001269182-A/2130.
Homo sapiens (human)
Homo sapiens
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PC C12P7
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BD025884
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Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z. Cancer gene determination and therapeutic screening using signature gene sets
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                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Avalon Pharmaceuticals (US)
Location/Qualifiers
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Sequence 5677 from Patent WO0194629.
AX335168.1 GI:18125887
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Oamlggsteelrvrlashlrklrrilrdpddlgkrlavyqagaregaerglsairer
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Patent: WO 9712992-A 28 10-APR-1997;
ROYAL NETHERLANDS ACADEMY OF A (NL.)
Other publication AU 7142796 970428.
Location/Qualifiers
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PATENT: WO 9712992-A 30 10-APR-1997;
ROYAL NETHERLANDS ACADEMY OF A (NL)
Other publication AU 7142796 970428.
Location/Qualifiers
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               PAT 20-JUN-2002
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                                                                                                               Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Tang, Y.T., Goodrich, R.W., Asundi, V. and Drmanac, R.T. Cathepain V-like polypeptides
Patent: US 6969-A 876 31-AUG-2004;
Nuvelo, Inc.; Sunnyvale, CA
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AR578700
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Sequence 38 from Patent WO0121836.
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AX427528.1 GI:21537674
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6660 118 0 0 0		AlaGlyCysGlnAla	GCAGGATGCCAGGCC
Length: Matches: Conservative: Mismatches: Indels:	(1-660)	1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18	62 ATGAAGGTTCTGTGGGCTGCGTTGCTCGTCCTGGCAGGATGCCAGGCC 115
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Search completed: June 14, 2006, 21:46:04 Job time : 560.375 secs

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Adc69792 Partial h
Adg71903 Human CDN
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Adg6961 Human tum
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Aad22047 Human apo
Aad22041 Human apo
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ADG71915
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(ASFR-) ASSOC FR CONTRE MYOPATHIES.
(TZRA/) TZARTOS S.
(MAMA/) MAMALAKI A.
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myasthenia gravis; ss; primer
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ADE15845;
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-YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
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Aav08172 Primer fo
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                                                                 June 14, 2006, 18:51:12; Search time 61.9495 Seconds (without alignments) 3038.776 Million cell updates/sec
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        GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                               - nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing First 45 summaries
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Database :

Result No.

Minimum DB Maximum DB

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New isolated human matrix metalloprotease gene - used to develop products for the diagnosis, prevention and treatment of e.g. cancer, arthritis or inflammation.
                                                                                                                                           Producing recombinant domains of the human muscle nicotinic acetylcholine receptor (AChR) for treating myasthenia gravis, which contains the major part of the extracellular domain of the AChR receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MMP19; matrix metalloprotease 19; human; cancer; arthritis; inflammation; therapy; diagnosis; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                      The present invention relates to producing of a group of recombinant domains of the human muscle nicotinic acetylcholine receptor (AChR) subunites alpha, beta, gamma, delta and epsilon, or the mutant forms of the molecules, or the alpha domain containing the P3A exon, which contains the major part of the extracellular domain of the receptor. The method is useful for producing recombinant domains of the human muscle nicotinic AChR for the immunosadoxption of anti-AChR antibodies in myasthenia gravis patients. The permanently immobilized molecules can be used atther separately or in combination for therapeutic in vitro or exvivo elimination/apheresis of the majority of the anti-AChR antibodies from the blood or sera of MG patients. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence 79 BP; 13 A; 23 C; 27 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V 1 0 0 0 0
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Matches:
Conservative:
Mismatches:
                         Psaridi-Linardaki L,
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                                                                                                                                                                                                                                                                          Example 4; SEQ ID NO 13; 28pp; English.
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92.00
100.0%
100.0%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               primer of the invention.
                            Mamalaki A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-531521/45.
                                                                                     WPI; 2003-903165/82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
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DB:
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The sequence represents a PCR primer used in the invention to amplify DNA encoding the clone 907334 matrix metalloprocease protein (MMP-ABT) from a plasmid. The invention relates to a novel polynucleotide, which comprises a nucleotide sequence encoding a human matrix metalloprocease protein (designated MMP-ABT). The protein of the invention has cytostatic, anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein, useful for diagnosing, inflammatory diseases (e.g. for treating these diseases.
                                   This sequence represents a PCR primer for the human matrix metalloprotease 19 (MMP19) coding sequence of the invention. The DNA, protein, and antibodies against MMP19 can be used in the diagnosis, prognosis, prevention or treatment of individuals with conditions associated with the expression of the MMP19 gene, such as cancer, arthritis or inflammation, or to identify a predisposition to these conditions. The DNA can be fixed to a substrate and used to detect the presence of MMP19 in a sample. The sequences can be used to make primers for use in reverse transcription PCR to detect MMP19, they can also be used to identify inhibitors of MMP19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human matrix metalloprotease protein MMP-ABT EST upstream PCR primer #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, MMP-ABT; matrix metalloprotease; cytostatic; anti-inflammatory; anti-arthritic; gene therapy; cancer; inflammatory disease; arthritis; EST; expressed sequence tag; PCR; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetlysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla
                                                                                                                                                                                                                              Sequence 93 BP; 22 A; 21 C; 27 G; 23 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                 Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                     (1-93)
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              Example 3; Page 49; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Page 23; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                     US-09-827-854A-13 (1-18) x AAV08172
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92.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (FALD/) FALDUTO M T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-361182/39
                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
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inflammatory, and anti-arthritic activity. The polynucleotide may have a use in gene therapy. The MMP-ABT polynucleotides and proteins are useful for detecting, diagnosing, staging, monitoring, prognosing, preventing or treating cancer or inflammatory diseases (e.g. arthritis). The MMP-ABT proteins and polynucleotides are also useful developing therapeutic agents that affect MMP function
   8866666688
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Sequence 93 BP; 22 A; 21 C; 27 G; 23 T; 0 U; 0 Other;

0000 Length: Matches: Conservative: Mismatches: Indels: 5.1e-07 92.00 100.0% 100.0% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: DB:

(1-93)US-09-827-854A-13 (1-18) x ABL57678 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC BP. ACD95309 standard; cDNA; 333 ACD95309; ACD95309 ò

69

Human colon cancer cell expressed cDNA #3721. 23-SEP-2003 (first entry)

breast cancer; population genome analysis; genetic shift; cancer; antibiotic resistance; antibiotic non-tolerance; congenital disease; agriculture; food crop genome; resistance gene; retrovirus; influenza virus; eukaryotic pathogen detection; trypanosome; Plasmodium; Open reading frame detection; genome sequencing; colon cancer; gene; ss.

Homo sapiens

JS2002155438-A1

24-OCT-2002

99US-00406117. 27-SEP-1999; 98US-00196716 20-NOV-1998;

SIMP/) SIMPSON A J G. (NETO/) NETO E D. (BREN/) BRENTANI R R. Brentani RR; Neto ED, Simpson AJG,

WPI; 2003-182626/18.

Determining open reading frames of genome of an organism e.g. a human suffering from cancer involves use of single oligonucleotide primer at low stringency for preparing single-stranded cDNA from mRNA of individual.

Example 9; Page 543; 959pp; English.

The invention describes a method of determining open reading frames in the genome of organism, comprising contacting mRNA from cell of organism with a single oligonucleotide primer (I) at low stringency, preparing single-stranded cDNA by reverse transcribing mRNA with (I), amplifying cDNA, sequencing the product, and repeating the contacting, preparing and amplifying steps with different primers and sequencing resulting nucleic acids. The method is useful for: determining that a known nucleotide sequence from a genome of an organism corresponds to a

conclected sequence of an open reading frame; for preparing a contig, nucleic acid molecule from a genome of an organism, and for sequencing connucles as the property of a genome of an organism. mRNA is obtained from mammalian or human cell which is associated with a pathological condition e.g. a colon cancer or breast cancer cell. The method is useful for analyses of large or small populations. further, it can be used to study living systems to determine if, e.g. there have been genetic shifts which render in individual or population more or less likely to be afflicted with congenited diseases, and the risk of affliction to a foetus, as well as the study of whether the conditions are likely to be passed to offspring through ova or sperm. The analyses for pathological conditions can be through ova or sperm. The analyses for pathological conditions can be carried out in all animals, plants, birds, fish, etc. Using this method, in the area of agriculture, for example the genomes of food crops can be studied to determine if resistance genes are present, defects in plant contained to determine if resistance genes are present, defects in plant contained to determine if resistance genes are present, defects in plant contained to determine if resistance genes are present, section as retroviruses and other integrating viruses such as influenza virus, have undergone shifts or mutations, which may require different approaches to therapy. This method is also applied to euwaryotic pathogens; such as cryptanosomes, different types of lasmodium, etc. The method essentially contained to the determination of the order of euwaryotic pathogens and other integrating viruses such as influences and elementing of non-coding portions. This method essentially and the pathogens of lasmodium, etc. The method essentially contained to the pathogens of lasmodium, etc. The method essentially contained to the pathogens of lasmodium, etc. The method essentially contained to the pathogens of lasmodium, etc. The method essentially contained to polynucleotide isolated from human colon cancer cell cDNA library

Sequence 333 BP; 73 A; 83 C; 120 G; 55 T; 0 U; 2 Other;

333 18 0 0 0 Length: Matches: Conservative: Mismatches: Indels: 2.26e-06 92.00 100.0% 100.0% 100.0% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: Pred. No.: Score:

US-09-827-854A-13 (1-18) x ACD95309 (1-333)

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S RESULT

AAC02139 standard; cDNA; 405 BP.

(first entry)

06-OCT-2000

Human secreted protein 5' EST, SEQ ID NO: 2137.

numan; 5' BST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.

Homo sapiens.

EP1033401-A2

06-SEP-2000.

21-FEB-2000; 2000EP-00200610

99US-0122487P 26-FEB-1999;

(GEST) GENSET

Giordano Duclert A, n, Dumas Milne Edwards

WPI; 2000-500381/45 P-PSDB; AAG02133

New nucleic acid that is a 5' expressed sequence tag (5' EST) for

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diagnostic, forensic, gene therapy and chromosome mapping procedures.
cDNAs and genomic DNAs that correspond to 5'ESTs and for
 obtaining
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Claim 1; SEQ ID NO 2137; 71pp + Sequence Listing; English.

The present sequence is one of a large number of 5' ESTB derived from mRNAs encoding secreted proteins. An ORP has been identified within the sequence. The 5' ESTB were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTB are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTB are derived from mRNAs with inteact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTB are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain uppercram regulatory sequences and to design expression and secretion vectors

Sequence 405 BP; 90 A; 105 C; 149 G; 60 T; 0 U; 1 Other;

405 000 000 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 2.85e-06 100.0% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match DB:

US-09-827-854A-13 (1-18) x AAC02139 (1-405)

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ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 128 1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18

ABK34238 standard; cDNA; 407 BP (first entry) 08-MAY-2002 ABK34238; RESULT

Human cDNA for novel secreted protein, SEQ ID 7.

diabetes; allergy; asthma; neurodegenerative disease; Crohn's disease; Alzheimer's disease; Parkinson's disease; liver fibrosis; tumour; coagulation disorder; haemophlia; inflammatory disorder; ulcer; tiseue regeneration; wound healing; haematopolesis; myeloid deficiency; Human, 88, gene, secreted protein, immune deficiency, viral infection, bacterial infection, fungal infection, autoimmune disorder, burn, rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis, lymphoid cell deficiency

Homo sapiens

WO200177290-A2.

18-OCT-2001.

29-MAR-2001; 2001WO-US010295

06-APR-2000; 2000US-0194941P

(GEMY) GENETICS INST INC

Agostino MJ, Fechtel K, JR; Wong GG, Clark HF, Gulukota K, Graham

WPI; 2002-179323/23.

Six hundred and twenty five polynucleotides derived from a variety of

The invention relates to 625 polynucleotides which have been derived from a variety of human tissue sources and which encode novel secreted corrected that complements and sequences that hybridise to them. Also included are a vector comprising the polynucleotide, a host cell transformed with the vector, the proteins encoded by the polynucleotides, antibodies that bind to the proteins and identification of modulators of the proteins or the expression of the polynucleotide. The polynucleotides can be used as probes for the identification and isolation of full length con be used as probes for the identification and isolation of full length con as nutritional supplements. The polynucleotides and proteins can also be used as nutritional supplements. The protein is useful in the treatment of various immune deficiencies and gloorders such as viral infections, bacterial infections, fungal infections, autoimmune thyroiditis and chanced arthritis, multiple sclerosis, autoimmune thyroiditis and disected also useful for treating neurodegenerative diseases (e.g. Alzheimer's also useful for treating neurodegenerative diseases (e.g. Alzheimer's can also useful for disease, liver fibrosis, coagulation disorders coan din the treatment of burns, inclaions and ulcers. The proteins are also useful for regulating haematopoiesis for treating myeloid or lymphoid cell deficiencies. The present sequence is one of the 625 cDNA coagulating a secreted protein useful for treating disorders. human tissue sources which encode secreted proteins, immune deficiencies and disorders such as autoimmune Claim 1; Page 70; 339pp; English.

Sequence 407 BP; 88 A; 103 C; 158 G; 58 T; 0 U; 0 Other;

407 000 000 000 Length:
Matches:
Conservative:
Mismatches: 2.86e-06 92.00 100.0% 100.0% Similarity: Percent Similarity: Alignment Scores: Query Match: Best Local

US-09-827-854A-13 (1-18) x ABK34238 (1-407)

18 73 1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 50 용 ð

ADV76096 standard; DNA; 440 BP. ADV76096

RESULT

ADV76096;

(first entry) 10-MAR-2005

NO 2937. Human colon tumor cell downregulated gene SEQ ID ds; gene; cancer; neoplasm; cytostatic.

Homo sapiens.

WO2004110345-A2.

23-DEC-2004.

28-OCT-2003; 2003WO-US034019.

29-OCT-2002; 2002US-0422176P.

(PHAA) PHARMACIA CORP.

Resnick RJ;

HOWER SH,

Hippenmeyer PJ, Bu JJ, Head RD, A, Staten NR; Bourner MJ, Bu Mazzarella RA,

Klein BK;

WPI; 2005-039958/04.

Matches:

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RESULT 9
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                                                            The invention relates to an antibody immunospecifically binds to peachbring fragment. The antibody is useful in preparing a composition for treating or preventing a cancer-associated disorder. The present sequence represents a gene downregulated in human colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an antibody immunospecifically binds to p-cadherin or its fragment. The antibody is useful in preparing a composition for treating or preventing a cancer-associated disorder. The present sequence represents a gene downregulated in human colon cancer
New antibody that immunospecifically binds to p-cadherin, useful in preparing a composition for treating or preventing a cancer-associated disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antibody that immunospecifically binds to p-cadherin, useful in preparing a composition for treating or preventing a cancer-associated disorder.
                                                                                                                                                                                                                               Human colon tumor cell downregulated gene SEQ ID NO 2936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klein BK
                                                                                                                   94 A; 114 C; 168 G; 62 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; 166 G; 62 T; 0 U; 0 Other,
                                                                                                                                              440
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                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
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                                           ID NO 2937; 257pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 2936; 257pp; English.
                                                                                                                                                                                   Indels:
                                                                                                                                                                                                                                                                                                                                                               gene; cancer; neoplasm; cytostatic.
                                                                                                                                                                                                              (1-440)
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                                                                                                                                                                                                                                                                                      ADV76095 standard; DNA; 441 BP
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                                                                                                                                             3.13e-06
92.00
100.0%
100.0%
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A, Staten NR;
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                                                                                                                                                                                                                                                                                                                           10-MAR-2005 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2005-039958/04.
                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                   BP;
                                           SEO
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Mazzarella RA,
                                                                                                                   Sequence 440
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Pred. No.:
                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                           Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                      23-DEC-2004
                                                                                                                                                                                  Query Match:
DB:
                                                                                                  cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cells.
                                                                                                                                             Pred. No.:
                                                                                                                                                                                                                                                                                                                                                               ds;
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The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of G SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences or each sequence tags (EST) for cidentifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations in esponsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antisense bnA or RNA. The purified polypeptide is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expressed sequence tag;
                                                                                                                                                                                                                Jones LW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 445 BP; 98 A; 113 C; 161 G; 72 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from USPTO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dickson MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seqdata.uspto.gov/sequence.html?DocID=20030073623
                         Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; ss; sequencing by hybridisation; SBH; ex
genome mapping; biodiversity; genetic disorder.
                                                                                     Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stache-Crain B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 8875; 44pp; English.
                                                                                                                                                               (1-441)
                                                                                                                                                                                                                                                                                                                                                                                     BP
                                                                                                                                                               US-09-827-854A-13 (1-18) x ADV76095
                                                                                                                                                                                                                                                                                                                                                                                  ACH21663 standard; cDNA; 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUL-2001; 2001US-00918995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUL-2001; 2001US-00918995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human adult ovary cDNA #43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
92.00
100.0%
100.0%
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LABAT I.
STACHE-CRAIN B
DICKSON M C.
JONES L W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drmanac RT, Labat I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antisense DNA or RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-615964/58.
                   Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                        ACH21663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DRMA/) I
(LABA/)
(STAC/)
(DICK/)
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Alignment Scores:

441

Length:

3.14e-06

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03-OCT-2000; 2000US-0237604P.
03-OCT-2000; 2000US-0237606P.
03-OCT-2000; 2000US-0237608P.
01-NOV-2000; 2000US-024508PP.
                                          (AVAL-) AVALON PHARM.
                                                                            WPI; 2002-188264/24.
                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200194629-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAY-2002
                                                    Young PE, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-DEC-2001
                                                                                                                                                                                                                                                                               Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                            ABL62679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene; ds.
                                                                                                                                                                                                                                                                                                                  Query Match:
                                                                                                                                                                                                                                                     tumour
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                                                                                                                                                               Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                               444
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                                                                                                                                                   Thyroid cancer related gene sequence SEQ ID NO:5677.
 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                  US-09-827-854A-13 (1-18) x ACH21663 (1-445)
                                                                                                          BP.
                                                                                                                                                                                                                                                                         2000US-0233617P.
2000US-0234617P.
2000US-0234034P.
2000US-0234034P.
2000US-0234034P.
2000US-0234034P.
2000US-0234034P.
2000US-0234034P.
2000US-023504P.
                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0236111P.
2000US-0236842P.
2000US-0236891P.
                                                                                                                                                                                                                                              30-MAY-2001; 2001WO-US010838
3.18e-06
92.00
100.0%
100.0%
                                                                                                         ABL67340 standard; DNA; 478
                                                                                                                                     15-MAY-2002 (first entry)
               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                  WO200194629-A2.
                                                                                                                                                                                                                                                                              27-SEP-2000; 2
27-SEP-2000; 2
28-SEP-2000; 2
28-SEP-2000; 2
28-SEP-2000; 2
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28-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                     25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
26-SEP-2000;
                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                13-DEC-2001
                                                                                                                        ABL67340;
                                                                                                                                                                                        gene; de.
                             Query Match:
DB:
  Pred. No.:
                                                                                            RESULT 10
                                                                                                     ABL67340/
           Score:
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The present invention describes a method (M1) for screening for an antineoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in comprises a sequence (S) selected from 847 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gane inerapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result to M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarinoma, calear call cancer, aquamous call carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
                                                                                                                                                    Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
Endress G, Horrigan S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Colon adenocarcinoma related gene sequence SEQ ID NO:1016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 478 BP; 72 A; 180 C; 123 G; 101 T; 0 U; 2 Other;
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118
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Matches:
Conservative:
Mismatches:
Indels:
Ebner R,
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                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 5677; 44pp; English.
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Carter KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABL62679 standard; DNA; 478 BP.
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92.00
100.0%
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Augustus M,
                                     Weaver Z;
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478 118 0 0 0

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Claim 1; SEQ ID NO 1016; 44pp; English
                                                                                                                   2000US-0235840P.
2000US-0235863P.
                                                          2000US-0234567P
                                                                                                              2000US-0235720P
                                                                                                                              2000US-0236028P
                                                                                                                                   2000US-0236032P
                                                                                                                                                                                                        2000US-0237425P.
2000US-0237598P.
     30-MAY-2001; 2001WO-US010838
                                     2000US-0234009P
                                                                                                                                                    2000US-0236109P
                                                                                                                                                         2000US-0236111P
                                                                                                                                                                              2000US-0237173P
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                                                                                                                                                                                                                                                              Augustus M,
                                                                                                                                                                                                                                                                   Weaver Z;
                                                                                                                                                                                                                                                   (AVAL-) AVALON PHARM.
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                                                                                                                                                                 29-SEP-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
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2-0CT-2000;
3-0CT-2000;
3-0CT-2000;
                                                    22-SEP-2000;
22-SEP-2000;
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                                                                                                              27-SEP-2000;
                                                                                                         -SEP-2000
                                                                                                                                                                                                                                                             Young PE, 1
Soppet DR,
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cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
tumour
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                drug toxicity, drug efficacy and drug metabolism. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fighthlished not seminary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a liver tissue sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 396 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 343
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
                                                                                                                          Sequence 478 BP; 72 A; 180 C; 123 G; 101 T; 0 U; 2 Other;
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                                                                                                                                                                                                     Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                  Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene #2492 used to diagnose liver cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 2492; 298pp; English.
                                                                                                                                                                                                                                                                                                                                                                                  US-09-827-854A-13 (1-18) x ABL62679 (1-478)
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ABN95994 standard; DNA; 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alvares C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-426119/45.
                                                                                                                                                                                                                                                                                    Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200229103-A2
                                                                                                                                                                                                                                                       Percent Similarity:
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                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-APR-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Horne D,
                                                                                                                                                                                                                                                                                                          Query Match:
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No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABN95994,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a method (M1) for screening for an antinopplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gne (I) of a signature gene set, where (I) comprises a sequence (S) selected from 847 sequences (given in AbL61664 to AbL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
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Sequence 478 BP; 72 A; 180 C; 123 G; 101 T; 0 U; 2 Other;

custom

least one custo PCR and RT-PCR

4 4 0 0 0 0 8 0 0 0 0

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for the custom assays, and delivering to the consumer at least one cu or stock assay in response to the order. The methods use PCR and RT-P procedures. The present sequence represents a human apolipoprotein E (apoE) DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                            Human diagnostic and therapeutic molecule; dithp; gene therapy; thalassemia; cardiovascular disorder; cell proliferative disorder; cancer; neurodegenerative disorder; autoimmune disorder; inflectious disorder; inflammatcry disorder; developmental disorder; Incyte ID number 3465999dec; secreted and extracellular molecule; ss.
                                                                                                                                                                                                                  Human diagnostic and therapeutic (dithp) cDNA sequence #38.
                                                                 Sequence 480 BP; 99 A; 137 C; 178 G; 66 T; 0 U; 0 Other;
                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                              AAS03049 standard; cDNA; 499 BP
                                                                                                                                                                                            US-09-827-854A-13 (1-18) x ADJ57602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0155760P.
99US-0155293P.
99US-0156524P.
99US-0156524P.
99US-016654P.
99US-016752P.
99US-016752P.
99US-016752P.
99US-016752P.
99US-016752P.
99US-016752P.
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99US-0168611P.
99US-0168613P.
99US-0168857P.
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92.00
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                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200121836-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 - SEP - 1999;
24 - SEP - 1999;
28 - SEP - 1999;
28 - SEP - 1999;
28 - SEP - 1999;
24 - NOV - 1999;
24 - NOV - 1999;
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24-NOV-1999;
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29-NOV-1999;
30-NOV-1999;
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                                                                                            Alignment Scores:
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01-DEC-1999;
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                                                                                                                     Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention provides methods and assays for ordering assays which detect single nucleotide polymorphisms (SNPs) or gene expression. It provides to a consumer, assays to detect presence or expression of genetic material, by providing a web-based user interface to receive an order for one or more stock assays, providing a web-based user interface to receive a request for design of one or more custom assays and an order
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Providing to consumer, assays for presence/expression of genetic material, by providing web-based user interface to receive order for stock assays, request for design and order for custom assays, and delivering assay.
                                                                                                                                                              1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; gene expression; genotyping; apolipoprotein E; apoE; human; gene; ds.
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                Human apolipoprotein E DNA sequence.
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                                                                                                                     US-09-827-854A-13 (1-18) x ABN95994
                                                                                                                                                                                                                       BP.
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2002US-0352356P.
2002US-0369127P.
2002US-0369657P.
2002US-0370921P.
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2002US-0380657P
2002US-0383654P
2002US-0383954P
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2002US-0394115P
2002US-0394115P
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                              3.45e-06
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                                                        Percent Similarity:
Best Local Similarity:
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28-JAN-2002;
01-APR-2002;
03-APR-2002;
09-APR-2002;
06-MAY-2002;
28-MAY-2002;
29-MAY-2002;
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Banville SC;

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., Dufour GE, Cohen HJ, Rosen BH, Shah P, Chalup MS;
Jones AL, Yu JY, Greenawalt LB, Panzer SR, Roseberry
Chen W, Liu TF, Yap PE, Stockdreher TK, Amshey S;
    Bratcher SR,
                                          RJ,
                        Hillman JL,
                                                                Fong WT;
                                              Wright
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WPI; 2001-281607/29.

Novel diagnostic and therapeutic polynucleotides, used in disease diagnosis and for gene therapy of conditions such as cancer and thalassemia.

Claim 1; Page 274; 299pp; English.

The present sequence for human diagnostic and therapeutic (dithp) cDNA sequence #38 is 1 of 71 (AAS03012-AAS03082) novel sequence #38 is 1 of 71 (AAS03012-AAS03082) novel sequences described in the invention. The present sequence (Incyte ID No: 345699960e) encodes a secreted and extracellular molecule. The dithp polymucleotides may be used to diagnose a condition disease or disorder associated with human colecules. They can be used to identify the presence of similar nucleic acids. Dithp polymucleotides may used to generate hybridisation probes for use in chromosomal mapping. Polypeptides (DITHP) encoded by dithp are used to screen for molecules which bind to them and modulate their used to screen for molecules and the used for gene therapy of disorders such as severe combined immunodeficiaency syndrome (SCID), cystic fibrosis, thalassemia, haemophilia resulting from Factor VIII or IX deficiencies, cardiovascular disorders e.g familial hypercholesrenchaemia (FH), cell proliferative disorders e.g cancers, neurodegenerative disorders e.g. cancers, infectious disorders and developmental disorders. The antibodies can be used to analyse protein expression levels

Sequence 499 BP; 107 A; 134 C; 189 G; 69 T; 0 U; 0 Other;

Length: Matches: Conservative: Mismatches: Indel8: 3.63e-06 92.00 100.0% 100.0% 100.0% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: Score:

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US-09-827-854A-13 (1-18) x AAS03049 (1-499)

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RESULT 15 ABZ11994

ABZ11994 standard; cDNA; 583 BP

ABZ11994;

(first entry) 20-JAN-2003 Human polynucleotide SEQ ID NO 876.

Human; genome mapping; gene therapy; food supplement; virus; fungus; cell-proliferative disorder; neurodegenerative disease; bacterial; parkinson's disease; Alzheimer's disease; autoimmune disease; multiple sclerosis; diabetes; genetic disorder; wound; burn; infection; multiple sclerosis; immunomodulator; nootropic; neuroprotective; arthitis; cytostatic; immunomodulator; nootropic; neuroprotective; antiparkinsonian; antidiabetic; immunosuppressive; dermatological; haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide; antiarthritic, gene, ss

Homo sapiens

12-SEP-2002.

05-MAR-2002; 2002WO-US005095.

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The invention relates to an isolated polynucleotide (I) comprising a nucleotide sequence selected from any of 948 sequences (ABZ1119-ABZ12066) or their mature protein coding portion, active domain coding protein or complementary sequences. The polynucleotides are useful for identifying expressed genes or for physical mapping of human genome. The coronded polypeptides (ABR68902-ABR66849) are useful as molecular weight markers, as a food supplement, for generating antibodies, in medical imaging, screening and diagnostic assays and for treating cellinaging, screening and diagnostic assays and for treating cellinaging, or Alzheimer's disease), autoimmune diseases (multiple sclerosis, diabetes, lupus) genetic disorders, myeloid or lymphoid disorders, collatelet or coagulation disorders, wound, burns, incision, ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal, parasitic), arthritis, etc. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                        New polynucleotides comprising sequences assembled from expressed sequence tags (ESTS), useful for treating cell-proliferative, neurodegenerative, automimune, genetic, myeloid or lymphoid, or platelet or coagulation disorders.
                                                                                                      Ren F;
                                                                                                    Zhao QA, R
, Ghosh M;
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                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 876; 1012pp + Sequence Listing; English.
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                                                                                                    Zhang J, Zl
R, Wang Z,
                                                                                               Goodrich RW, Asundi V, Zhe
a Y, Yamazaki V, Chen R,
Wang D, Drmanac RT;
                                                                                                      Goodrich RW,
                  05-MAR-2001; 2001US-00799451
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                                                                                                                         Xue AJ, Yang Y, Ma
Wehrman T, Wang J,
                                                           (HYSE-) HYSEQ INC.
                                                                                                      Zhou P,
                                                                                                                                                                                                               P-PSDB; ABP69777
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583 0 0 0 0 0 Length: Matches: Conservative: Mismatches: Indels: 92.00 100.0% 100.0% Percent Similarity: Best Local Similarity: Query Match: Score:

Alignment Scores:

(1-583)US-09-827-854A-13 (1-18) x ABZ11994

56 AIGAAGGTTCTGTGGGCTGCTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 109 1 MetlysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla

Search completed: June 14, 2006, 19:10:36 Job time : 64.9495 secs

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CN277382 170004248
BB766766 IL3-NT010
BM845846 K-EST0124
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A1910041 RC-BT234-
CN277368 170005319
AN383864 QV3-HT036
CN277382 170005315
BP418358 BP418358
BQ684487 AGENCURT
DV770547 ILLUMIGEN
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AV686644 AV686644
AI347700 GDOLIL:X
AI277384 170005315
CN277411 170005315
AI31109 GO92a10:X
AI311109 GO92a10:X
AI311109 GO92a10:X
AV68587 AV68587
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AV684377 AV684377
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QV1-HT047
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1 (bases 1 to 125)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L. W.
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Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
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           GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                   nucleic search, using frame_plus_p2n model
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Site 2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of Lissue mRNA and cDNA amplification were performed under low stringency conditions."
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1 (bases 1 to 216)

Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M.S., Mandalam, R., Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)
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Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025,
Tel: 650 473 8658
Fax: 650 473 7760
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                             1. .125
//organism="Homo sapiens"
//organism="Homo sapiens"
//organism="Homo sapiens"
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from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 177)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagaal, M.A., achdin, S., Coste, F., Ragaal, M.A., Garcia, C., Coste, F., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 bp mRNA linear EST 17-JAN-2001 QV2-ET0106-161100-475-f12 ET0106 Homo sapiens cDNA, mRNA sequence. BF877359 GI:12267489 EST.
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Fax: +55-11-2707001

Faxi. +55-11-2707001

This sequence was darived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=GV2&t2=QV2-ET0106-IS100-475-f12&t3=2000-11-16&t4=1)
Seg primer: puc 18 forward
High quality sequence stop: 177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shorgun sequencing of the human transcriptome with ORF expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .177
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/note="Organ: lung_tumor; Vector: puc18; Site_1: Smal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
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Matches:
Conservative:
Mismatches:
Indels:
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         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                             6.07e-06
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                               Pred. No.:
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AUTHORS
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BF877359
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

PUBMED JOURNAL

COMMENT

TITLE

FEATURES

RESULT 4 BF877229/c

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DEFINITION

LOCUS

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Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Parent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
                                                                                                                                                                                                                                        Hominidae, Homo.

1 (bases I to 221)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Brass, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,

O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-ET0106-161D0-475-b06&t2=2000-11-16&t4=1)
Seq primer: puc 18 forward
High quality sequence.stopp: 221.
  BF877344 221 bp mRNA linear EST 17-JAN-2001
QV2-ET0106-161100-475-b06 ET0106 Homo sapiens cDNA, mRNA sequence.
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                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
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                                                                                 BF877344.1 GI:12267474
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                                                                                                                                      Homo sapiens (human)
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SOURCE
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AUTHORS
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/ organism="Homo sapiens"
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/ dev_stage="RAULt"
/ clone lib=="ET0106"
/ note="Organ: lung tumor; Vector: puc18; Site_l: Smal;
/ note="Organ: lung tumor; Vector: puc18; Site_l: Smal;
/ note="Organ: lung ini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae, Homo.

1 (Dases 1 to 221)

Dias Neto, E., Garcia, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Sllva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,

O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                             BF877229 221 bp mRNA linear EST 17-JAN-2001
QV2-ET0106-151100-478-b01 ET0106 Homo sapiens cDNA, mRNA sequence.
BF877229
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-ET0106-1100-478-bol&t2=2000-11-15&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 221.
                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shotgun sequencing of the human transcriptome with ORF expressed
195 Argaadgricrigriggecriccirigcriggrearinecriggeaggarigecaggee 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
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Best Local Similarity:
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Query Match:

Pred. No.:

ORIGIN

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Hominidae; Homo.

1 (bases 1 to 227)
Dias Neto,B., Garcia,R., Verjovski-Almeida,S., Briones,M.R.,
Dias Neto,B., Garcia, Correa,R., Verjovski-Almeida,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Mare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BI039120 227 bp mRNA linear EST 14-JUN-2001
IL3-NT0280-240101-418-F05 NT0280 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                             Tel: +55-11-2704922

Fax: +55-11-2707001

Email: saimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-ET0106-161100-474-gll&t3=2000-11-16&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 223.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                  Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rus Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                          Shorgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
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0 0 0 0 0
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Matches:
Conservative:
Mismatches:
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1 (Dases 1 to 223)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Costa,F.F., Goldman,G.H., Cavalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jorgeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BF877285 223 bp mRNA linear EST 17-JAN-2001
QV2-ET0106-161100-474-gl1 ET0106 Homo sapiens CDNA, mRNA sequence.
BF877285
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1. (Dases 1 to 223)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                     Pax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-ET0106-
141100-474-q911&t3=2000-11-14&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 223.
High quality sequence stop: 223.
              Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                   Concact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MetLygValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
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Paulo-SP,

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1. .230
/organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/dev_stage="Adult"
/clone lib="MT0280"
/note="Organ: nervous tumor; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
Gerived from ORESTES PCR (U.S. Letters Patent application
No. .196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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                                   Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation Nat. Biotechnol. 22 (6), 707-716 (2004)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CN277423 243 bp mRNA linear EST 16
17000425248791 GRN_ES Homo sapiens CDNA 5', mRNA sequence.
CN277423
  Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao
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Geron Corporation
230 Constitution Drive, Menlo Park, CA
Tel. 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 243 Std Error: 0.00.
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/mol_type="mRNA"
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1 (bases 1 to 243)
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                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
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/db xref="taxon:9606"
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/clone llb="mY0280"
/note="Organ: nervous tumor; Vector: pucl8; Site_l: Smal;
/note="Organ: nervous tumor; Vector: Patent application
/no. 196,716 - Ludwig Institute for Cancer Research)
/profiles into the pUC 18 vector: Reverse transcription of tissue mRNA and cDNA amplification were performed under
/low stringency conditions."
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1 (bases 1 to 210)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunc, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                               Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=LL3&t2=LL3-NT0280-
240101-418-POS&t3=2001-01-24&t4=1)
Seq primer: puc 18 forward

High quality sequence stop: 227.

Location/Qualifiers
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mRNA sequence.
                                             Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
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IL3-NT0280-090201-454-D05 NT0280 Homo sapiens cDNA,
BI040603
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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ORIGIN

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/db_Xref="Autor"
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/note="Organ: A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256 bp mRNA linear EST 21-JUN-2000 QV1-HT0471-280300-121-£07 HT0471 Homo sapiens cDNA, mRNA sequence. BE164912 BE164912.1 GI:8627633 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV1-HT0471-280
300-121-f07kt3=2000-03-28kt4=1)
Seq primer: puc 18 forward
High quality sequence start: 12
High quality sequence start: 12
High quality sequence stop: 256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

(Gases I to 256)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
tissue mRNA and cDNA amplification were performed under low stringency conditions."
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                                                                                                                                                                                                                                                                                                                                                                                     US-09-827-854A-13 (1-18) x BE164869 (1-256)
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Homo sapiens
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Best Local Similarity:
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BE164912
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV1-HT0471-270 300-121-f07&t3=200-03-27&t4=1)
Seq primer: puc 18 forward
High quality sequence stort: 12
High quality sequence stort: 12
High quality sequence story: 256.
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1 (Bases I to 256)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, P.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., Grimpson, A.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE164869 EST 21-JUN-2000 QV1-HT0471-270300-121-f07 HT0471 Homo sapiens cDNA, mRNA sequence. BE164869.1 GI:8627590
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H9"
                                                                                                  /clone_lib="GRN_ES"
/note="oligo dT primed, full-length enriched cDNA library from undifferentiated hES cell lines H1 (p32), H7 (p29), and H9 (p26) and anaintained in feeder-free conditions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shorgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-827-854A-13 (1-18) x CN277423 (1-243)
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Homo sapiens
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Best Local Similarity:
Query Match:
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AUTHORS
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Pred. No.:

LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

RESULT 13 CB153811

요 8

ORGANISM

TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS

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/clone_lib="ET0106"

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Site_2: Smal; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."
                                                                                                                                                                                       Hominidae, Homo.

1 (Dases 1 to 273)

Dias Neto,E., Garcia,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.,

Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
        BF877186 273 bp mRNA linear EST 17-JAN-2001
QV2-ET0106-151100-477-£05 ET0106 Homo sapiens CDNA, mRNA sequence.
BF877186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

Enail: asimpson@ludwig.org.br

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-ET0106-151100-477-f05&t2=2000-11-15&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 273.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    274 bp mRNA linear EST 17-JAN-2001 QV2-ET0106-151100-478-c04 ET0106 Homo sapiens cDNA, mRNA sequence. BF877232.1 GI:12267362 EST.
                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                                                              BF877186.1 GI:12267316
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BF877232
    3F877186
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21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
FS Beeun-dong Yuseong-gu, Daejeon 305-333, South Korea
                                                                                                                                                                                                                                                              269 bp mRNA linear EST 29-JAN-2003
K-EST02111405 L17N670205 Homo sapiens cDNA clone L17N670205-6-G09
5', mRNA sequence
CB153811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="ToploF'"

/clone lib="L17N670205"

/note="Organ: Liver; Vector: pT/T3D-PacI; Site 1: EcoRI;

Site_2: NotI; The library was contributed by the Soares

laboratory and it was constructed as described by Bonaldo,

A.F. Lennon, G. and Soares, M.B. (1996), Genome Research

6(9): 791-806. RNA was prepared from harvested cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: yongsung@mail.kribb.re.kr
Plate: 6 row: G column: 09
High quality sequence stop: 269.
Location/Qualiflers
                                                                                                                                     (1-256)
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                                                                                                                               US-09-827-854A-13 (1-18) x BE164912
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Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                              Percent Similarity:
Best Local Similarity:
Query Match:
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Query Match:

RESULT 14

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Pred. No.:

ORIGIN

us-09-827-854a-13.p2n.rst

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Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196, 716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
                                                                                            Hominidae, Homo.

1 (bases 1 to 274)

Diss Neto,E., Garcia, Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,

O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

Ensil: asimpson@ludwig.org.br

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-ET0106-15100-478-004&t3=2000-11-15&t4=1)

Agg primer: puc 18 forward

High quality sequence stop: 274.
Homo sapiens
Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                        Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
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Mismatches:
Indels:
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31, 1007, Ar Appli

1386, Ap 3, Appli

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Sequence 10, Application US/08148910

Patent No. 5466593

GENERAL INFORMATION:
APPLICANT: Takeshi SHIMOMURA et al.
TITLE OF INVENTION: No. 54665911 Protein and Gene Encoding Said Protein
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
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US-10-211-689-31
US-09-023-655-1007
US-09-023-655-1007
US-09-080-107-224
US-09-919-039-246
US-10-211-689-45
US-10-211-689-45
US-09-919-039-246
US-09-919-039-39
US-09-949-155-51
US-09-949-155-51
US-09-949-115-31
US-09-949-016-1779
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US-09-949-016-17344
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/148,910
FILING DATE: No. 5466593ember 5, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch,
MEDIUM TYPE: 500 Kb Storage
COMPUTER: IBM COMpatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367 REFERENCE/DOCKET NUMBER:
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STATE: D.C.
COUNTRY: U.8
ZIP: 20005
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US-08-148-910-10
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Sequence 2137, Ap
Sequence 2491, Ap
Sequence 876, App
Sequence 28, Appl
Sequence 29, Appl
                                                                                                                             June 14, 2006, 19:03:31; Search time 18.795 Seconds (without alignments) 2687.952 Million cell updates/sec
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| EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
| EMC_Celerra_SIDS3/ptodata/2/ina/6 COMB.seq:*
| EMC_Celerra_SIDS3/ptodata/2/ina/6 ECOMB.seq:*
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| EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
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                     GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                             OM protein - nucleic search, using frame plus p2n model
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US-08-448-937A-10
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US-09-513-9996-2137
US-09-880-107-2491
US-08-726-306A-28
US-08-726-306A-28
US-10-211-689-29
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Scoring table:

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51, Appl 51, Appl 7011, Ap 7153, Ap 2604, Ap 12815, A

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| Sequence 10, Application US/08448937A
| Sequence 10, Application US/08448937A
| Patent No. 5677164
| Patent No. 5677164
| TILE OF INVENTION: No. 5677164el Protein and Gene Encoding Said Protein NUMBER OF SEQUENCES: 14
| CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Wenderoth, Lind & Ponack
| STREET: 805 Fifteenth Street, N.W., #700
| CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
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                                                                          INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 71 base pairs
TYPE: nucleic acid
STRANDEDNES: double
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid (synthetic DNA)
ORIGINAL SOURCE:
ORGANISM: human
                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
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CARPUTER READSHEE FORM:
MEDIUM TYPE: Diskette, 5.25 inch,
MEDIUM TYPE: Diskette, 5.25 inch,
MEDIUM TYPE: Diskette, 5.25 inch,
MEDIUM TYPE: DO KD SLORGE
COMPUTER: IBM COMPALIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,937A
FILING DATE: May 24, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/148,910
FILING DATE: NO. 56/7164ember 5, 1993
ATTORNEY/AGENT INFORMATION:
NAME: WALTEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
RESERENCE/DOCKET NUMBER:
TELEPHONE:
TELEPHONE: 202-371.8850
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
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SEQUENCE CHARACTERISTICS:
LENGTH: 71 Dame pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity:
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APPLICANT: Abbott Laboratories
APPLICANT: Falduto, Michael T.
APPLICANT: Falduto, Michael T.
APPLICANT: Falduto, Michael T.
APPLICANT: Magnuson, Scott R.
TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
TITLE OF INVENTION: OF USING SAME
FILE REFERENCE: 6073.US.Pl
CURRENT APPLICATION NUMBER: US/09/391,104
CURRENT APPLICATION NUMBER: US 08/814,394
PRIOR FILING DATE: 1997-03-11
PRIOR FILING DATE: 1997-03-11
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
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Matches:
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Mismatches:
Indels:
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                              Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              // Sequence 4, Application US/09391104
// Patent No. 6399371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
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Alignment Scores:
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396 Argaagerrcreredecrecerrecrestrecretrecrescassaristicas
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APPLICANT: Xue, Aidong J.
APPLICANT: Zhao, Qing A.
APPLICANT: Zhao, Qing A.
APPLICANT: Ama, Yunqing
APPLICANT: Mang, Yunqing
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Nonghong
APPLICANT: Parmanc, Radje T.
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Polypeptides
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: PL-L-Genes Version 2.0
LENGTH: S83
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118
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APPLICANT: van Leeuwen, Frederik Willem
APPLICANT: Burbach, Johannes Peter Henri
APPLICANT: Grosveld, Franklin G.
TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS
NUMBER OF SEQUENCES: 189
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: I Financial Center
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 28, Application US/08726306A; Patent No. 5958684; GENERAL INFORMATION:
                                                                                                                 ; Sequence 876, Application US/09799451; Patent No. 6783969; GENERAL INFORMATION:
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92.00
100.0%
100.0%
100.0%
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APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyan
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: CDS
; LOCATION: (100)..(423)
US-09-799-451-876
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Best Local Similarity:
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                                                                                RESULT 6
US-09-799-451-876
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US-09-880-107-2491/C
US-09-880-107-2491, Application US/09880107
Fatent No. 6974667
GENERAL INFORMATION:
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
TILE OF INVENTYON: Gene Expression Profiles in Liver Cancer;
TILE REFERENCE: 44921-5028-WO
CURRENT PELLING DATE: 2001-06-14
PRIOR FILING DATE: 2000-06-14
SPRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Genbank Accession No. 6974667 N33009 NAME/EXT: unamer (11)... (478) CATHER INFORMATION: n = a or c or g or t
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                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: UNSURE
LOCATION: 20
OTHER INFORMATION: Xaa=Glu or Gln
US-09-513-999C-2137
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                                                                        TYPE: DIA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 119..403
FEATURE:
NAME/KEY: misc_feature
LOCATION: 176
OTHER INFORMATION: s=g or c
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 2137
LENGTH: 405
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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Pred. No.:
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Pred. No.:
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FILE REFERENCE: 21402-416B

CURRENT APPLICATION NUMBER: US/10/211,689

CURRENT FILING DATE: 2003-01-21

PRIOR APPLICATION NUMBER: 60/311751

PRIOR APPLICATION NUMBER: 60/311751

PRIOR FILING DATE: 2001-08-08

PRIOR FILING DATE: 2001-08-09

PRIOR FILING DATE: 2001-08-09

PRIOR FILING DATE: 2002-08-09

PRIOR APPLICATION NUMBER: 60/361,159

PRIOR APPLICATION NUMBER: 60/361,159

PRIOR PLICATION NUMBER: 60/330,050

PRIOR PILING DATE: 2002-04-16

PRIOR FILING DATE: 2002-06-15

PRIOR FILING DATE: 2002-06-15

PRIOR FILING DATE: 2001-08-13

PRIOR FILING DATE: 2001-08-13

PRIOR FILING DATE: 2001-08-13

PRIOR FILING DATE: 2001-08-13

PRIOR PRILING DATE: 2001-08-13

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PRIOR PRILING DATE: 2001-08-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boldog, Ferencia.
Burges, Catherine E.
Casman, Stacie J.
Edinger, Shlomit R.
Gangolli, Esha A.
Gorman, Linda
Gow, Xiaojia (Sasha)
Khramstov, Nikolai V.
Lepley, Denise M.
MacDougall, John R.
Pena, Carol A.
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Patturajan, Meera
Rieger, Daniel K.
Shimkets, Richard A.
Smithson, Glennda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Aleobrook, John II
APPLICANT: Anderson, David W
APPLICANT: Boldog, Ferenc L.
APPLICANT: Burgess, Catherine E
APPLICANT: Casman, Stacie J.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Gangolli, Esha A.
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Khramstov, Nikolai V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.38e-07
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100.0%
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ORGANISM: Homo sapiens
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, LOCATION: (18)..(599)
US-10-211-689-29
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Best Local Similarity:
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US-10-211-689-41
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LENGTH: 684
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APPLICANT: Zhong, Mei
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 ATGAAGGTTCTGTGGGCTGCTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 115
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ZIP: 02111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage COMPUTER: IBM PC compatible OPERATION SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,306A
FILING DATE: 02-Oct-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/926
PRIOR APPLICATION DATE: 02-Oct-1995
PRIOR APPLICATION DATE: 02-Oct-1996
ATPLICATION NUMBER: US 60/009,832
FILING DATE: 01-Jan-1996
ATPLICATION NUMBER: US 60/009,832
FILING DATE: 01-Jan-1996
ATPLICATION NUMBER: 34,380
REPRERENCE/DOCKET NUMBER: 34,380
REPRERENCE/OCKET NUMBER: 34,380
REPRERENCE/DOCKET NUMBER: 34,380
TELEPHONE: (617) 345-9110
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 345-9111
INFORMATION FOR SED ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 660 base pairs
TYPE: nucleic acid
STRANDEDRESS: double
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Sequence 29, Application US/10211689
Patent No. 6974684
GENERAL INFORMATION:
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Khramstov, Nikolai V.
Lepley, Denise M.
MacDougall, John R.
Pena, Carol A.
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Burgess, Catherine E.
Casman, Stacie J.
Edinger, Shlomit R.
Gangolli, Esha A.
Gorman, Linda
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Alsobrook, John II
APPLICANT: Anderson, David W.
APPLICANT: Boldog, Ferenc L.
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Patturajan, Meera
Rieger, Daniel K.
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APPLICANT: Rieger, Daniel K.
APPLICANT: Shinkers, Richard A.
APPLICANT: Shinkers, Richard A.
APPLICANT: Shinkers, Richard A.
APPLICANT: Shinkers, Corine A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Vernet, Corine A. M.
APPLICANT: Vernet, Corine A. M.
APPLICANT: Vernet, Mai
TITLE REPRENCE: 21402-416B
CURRENT APPLICATION NUMBER: US/10/211,689
CURRENT APPLICATION NUMBER: US/310,795
FRIOR FILING DATE: 2001-08-10
FRIOR FILING DATE: 2001-08-09
FRIOR PRILOR DATE: 2001-08-09
FRIOR PRILOR APPLICATION NUMBER: 60/310,795
FRIOR PRILOR APPLICATION NUMBER: 60/311,292
FRIOR APPLICATION NUMBER: 60/311,292
FRIOR APPLICATION NUMBER: 60/311,599
FRIOR FILING DATE: 2002-08-09
FRIOR PRILOR DATE: 2002-08-16
FRIOR FILING DATE: 2002-08-16
FRIOR FILING DATE: 2002-08-16
FRIOR FILING DATE: 2002-08-16
FRIOR FILING DATE: 2002-08-16
FRIOR APPLICATION NUMBER: 60/381,309
FRIOR FILING DATE: 2002-08-16
FRIOR FILING DATE: 2002-08-16
FRIOR APPLICATION NUMBER: 60/381,309
FRIOR FILING DATE: 2002-08-16
FRIOR APPLICATION NUMBER: 60/381,309
FRIOR FILING DATE: 2002-08-16
FRIOR PRIOR APPLICATION NUMBER: 60/381,309
FRIOR FILING DATE: 2002-08-16
FRIOR PRIOR FILING DATE: 2002-08-16
FRIOR PRIOR PRIOR APPLICATION NUMBER: 60/381,309
FRIOR FILING DATE: 2002-08-16
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Edinger, Shlomit R. Gangolli, Esha A. Gorman, Linda Guo, Xiaojia (Sasha) Khramsrcov, Nikolai V. Lepley, Denise M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Alsobrook, John II
APPLICANT: Anderson, David W.
APPLICANT: Boldog, Ferenc L.
APPLICANT: Burgess, Catherine B.
APPLICANT: Casman, Stacie J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.52e-07
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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; NAME/KEY: CDS
; LOCATION: (2).
US-10-211-689-35
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                             APPLICANT: Vornet, Corine A. M.
APPLICANT: Vornet, Corine A. M.
APPLICANT: Stoney, Medi
TILLE REPERBUGE: 2009.9 Medi
FILE REPERBUGE: 21400-416B
FILE REPERBUGE: 21400-416B
FILE REPERBUGE: 21400-416B
FILE REPERBUGE: 2100-10-121
FILE REPERBUGE: 2003-01-21
PRIOR APPLICATION WUMBER: 60/311/51
PRIOR APPLICATION WUMBER: 60/310/395
PRIOR APPLICATION WUMBER: 60/310, 795
PRIOR APPLICATION WUMBER: 60/311, 292
PRIOR APPLICATION WUMBER: 60/311, 292
PRIOR APPLICATION WUMBER: 60/311, 292
PRIOR PLING DATE: 2001-08-09
PRIOR PLING DATE: 2002-04-08
PRIOR PLING DATE: 2002-04-08
PRIOR PLING DATE: 2002-04-08
PRIOR PLING DATE: 2002-04-16
PRIOR PLING DATE: 2002-06-15
PRIOR PLING DATE: 2001-09-31
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Mismatches:
Indels:
Gaps:
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Patent No. 6974684
GENERAL INFORMATION:
APPLICANT: Alsobrook, John II
APPLICANT: Anderson, David W.
APPLICANT: Burgess, Catherine E.
APPLICANT: Casman, Stacie J.
APPLICANT: Gangolli, Esha A.
APPLICANT: Gangolli, Esha A.
APPLICANT: Gorman, Linda
APPLICANT: Gorman, Linda
APPLICANT: Holdey, Denise M.
APPLICANT: HacDougall, John R.
APPLICANT: Pepley, Denise M.
APPLICANT: Pepley, Denise M.
APPLICANT: Pepley, John R.
APPLICANT: Pepley, John R.
APPLICANT: Pepman, John A.
APPLICANT: Peyman, John A.
APPLICANT: Peyman, John A.
                   Vernet, Corine A. M.
Voss, Edward Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.48e-07
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(709)
US-10-211-689-41
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Best Local Similarity:
Query Match:
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US-10-211-689-35
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LENGTH: 709
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APPLICANT: VOSS, Edward Z.
APPLICANT: VOSS, Edward Z.
APPLICANT: Slong, Mei
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHC.
FILE REFERENCS: 21402-416B
CURRENT APPLICATION NUMBER: US/10/211,689
CURRENT PILING DATE: 2001-03-01-21
PRIOR FILING DATE: 2001-08-08
PRIOR FILING DATE: 2001-08-08
PRIOR FILING DATE: 2001-08-08
PRIOR FILING DATE: 2001-08-08
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2002-02-28
PRIOR FILING DATE: 2002-04-16
PRIOR FILING DATE: 2002-05-15
PRIOR FILING DATE: 2002-05-15
PRIOR FILING DATE: 2002-05-16
PRIOR FILI
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Matches:
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Sequence 1007, Application US/09023655

Parent No. 6607879

GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Suean G. Stuart
APPLICANT: Jeffrey J. Seilhamer
                                           Guo, Xiaojia (Sasha)
Khramstov, Nikolai V.
Lepley, Denise M.
MacDougall, John R.
Pena, Carol A.
Peyman, John A.
                                                                                                                                                                                                                                   Patturajan, Meera
Rieger, Daniel K.
Shimkets, Richard A.
Smithson, Glennda
Spytek, Kimberly A.
Vernet, Corine A. M.
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ORGANISM: Homo sapiens
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Best Local Similarity:
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LENGTH: 802
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APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT: MacDougall, John R.
APPLICANT: Pena, Carol A.
APPLICANT: Pena, Carol A.
APPLICANT: Perman, John A.
APPLICANT: Perman, John A.
APPLICANT: Patturial m. Meera
APPLICANT: Shinkee; Richard A.
APPLICANT: Corine A. M.
APPLICANT: Organization Winbers: US10/211,689
CURRENT APLICATION NUMBER: US110/211,689
RRIOR APLICATION NUMBER: US1310,302
PRIOR APLICATION NUMBER: 60/310,795
PRIOR APLICATION NUMBER: 60/310,795
PRIOR APLICATION NUMBER: 60/310,795
PRIOR PLILNG DATE: 2001-08-08
PRIOR PLILNG DATE: 2001-08-03
PRIOR PLING DATE: 2001-08-03
PRIOR PRIOR PLING DATE: 2001-09-03
PRIOR PLING DATE: 20
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Sequence 31, Application US/10211689
Sequence 31, Application US/10211689
Sequence 31, Application US/10211689
GENERAL INFORMATION:
APPLICANT: Aleobrook, John II
APPLICANT: Boldog, Ferenc L.
APPLICANT: Burgess Catherine E.
APPLICANT: Gangun, Stacie J.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Gangolli, Esha A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.82e-07
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ORGANISM: Homo sapiens
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; NAME/KEY: CDS
; LOCATION: (18)..(704)
US-10-211-689-33
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Best Local Similarity:
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LENGTH: 788
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Query Match:
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         COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE EXPRESSION
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| Sequence 1, Application US/07709949 |
| Sequence 1, Application US/07709949 |
| Patent No. 5472858 |
| GENERAL INFORMATION: |
| APPLICANT: Attie, Alan D |
| APPLICANT: Gretch, Daniel G |
| APPLICANT: Sturley, Stephen L |
| APPLICANT: Beckage, Nancy E |
| TITLE OF INVENTION: Production of Recombinant Proteins in TITLE OF INVENTION: Insect Larvae |
| NUMBER OF SEQUENCES: |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: Quarles & Brady |
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLANDRES OF SEQUENCES: 1508

NUMBER OF SEQUENCES: 1508

CORRESPONDENCE ADDRESS:
ADDRESSE: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EPOPPY disk
COMPUTER: EPOPPY disk
COMPUTER: EPOPPY disk
COMPUTER: EPOPPY disk
COMPUTER: ENDABLE FORM:
MEDIUM TYPE: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELEPHONE: (650) 845-055
TELEPRAX: (650) 845-4166
INFORMATION FOR ERO ID NO: 1007:
SEQUENCE CHARACTERISTICS:
LENGTH: 1156 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
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STREET: P.O. Box 2113
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Best Local Similarity:
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STATE: WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-023-655-1007
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Pred. No.:
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DB:
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62 ATGAAGGITCTGTGGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 115
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Patent No. 6974667

GENERAL INFORMATION:

APPLICANT: Horne, Darci T.

APPLICANT: Scherf, Uwe

APPLICANT: Gene Logic, Inc.

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;
FILE REFERENCE: 44921-5028-WO

CURRENT APPLICATION NUMBER: US/09/880,107

CURRENT FILING DATE: 2001-06-14

PRIOR FILING DATE: 2000-06-14
COMPUTER: READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEB PC compatible
COMPUTER: IEB PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/709,949
FILING DATE: 19910604
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 96.29691801
TELECOMMUNICATION INFORMATION:
TELECHOME: (608) 251-5000
TELECHOME: (608) 251-9166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1157 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 1157
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Matches:
Conservative:
Mismatches:
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Journal of Biological Chemistry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
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ORGANISM: Homo sapiens
FEATURE:
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100.0%
100.0%
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PUBLICATION INFORMATION: AUTHORS: McLean, J W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 62..1015
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
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Best Local Similarity:
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VOLUME: 2
PAGES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
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Appli

Appli Appli Appli Appl

OM protein

Run on:

Sequence:

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Sequence 293', Ap Sequence 2936, Ap Sequence 8875, Ap Sequence 374, App Sequence 1016, Ap Sequence 1016, Ap Sequence 1016, Ap Sequence 1016, Ap Sequence 1016, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Appl
Sequence 106, App
Sequence 63, Appl
Sequence 5, Appli
Sequence 1, Appli
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Sequence 125, App
Sequence 1, Appli
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Sequence 1, Appli
Sequence 17, Appl
Sequence 1, Appli
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Sequence 2244, Ap
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Sequence 409, App
Sequence 3, Appli
Sequence 3278, Ar
Sequence 8950, A
Sequence 7, Appli
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Seguence 129, Apr
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| Sequence 4, Application US/09391104
| Publication No. US20020031817A1
| GENERAL INFORMATION
| APPLICANT: Abbott Laboratories
| APPLICANT: Falduto, Michael T.
| APPLICANT: Magnuson, Scott R.
| APPLICANT: Morgan, Dunglas W.
| TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS TITLE OF INVENTION: OF USING SAME
| FILE REFERENCE: 6073.US.Pl
| CURRENT PAPLICATION NUMBER: US/09/391,104
| CURRENT FILING DATE: 1999-09-07
| PRIOR FILING DATE: 1997-03-11
                           US-09-823-245A-7
US-10-696-639-2937
US-10-696-639-2936
US-09-918-995-8875
US-09-964 BSAA-374
US-09-880-107-2491
US-09-873-367C-1016
                                                                                                                              US-10-843-641A-1016
US-10-843-641A-5677
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US-10-937-758A-106
US-10-773-446-63
US-11-186-284-5
US-11-055-309A-1
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US-10-211-689-29
US-10-211-689-35
US-10-211-689-35
US-10-211-689-31
US-10-211-689-31
US-10-211-689-31
US-10-211-689-31
US-10-211-689-31
US-10-211-689-31
US-10-817-854-10
US-09-827-854-10
US-09-827-854-10
US-09-827-854-11
US-09-827-854-12
US-09-827-854-12
US-09-827-854-12
US-10-817-854-12
US-10-31-82-5
US-10-31-82-5
US-10-428-551-1
US-10-428-551-1
US-10-428-551-1
US-10-428-551-1
US-10-428-851-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
OTHER INFORMATION: Upstream primer
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 COmmand line parameters:

-MODEL=frame+_p2n.model -DEV=x1h
-Q= AbssRABSWEB spool/180982784/runat 14062006_081838_26978/app_query.fasta_1
-Q= AbssRABSWEB spool/1809827864/runat 14062006_081838_26978/app_query.fasta_1
-DB=Published_Applications NA Main -QFWT=fastap _SUFFIX=p2n.rnpbm
-MINAATCH=0.1 -LOOPCL=0 -LCOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=D10sung5 - TRANS=buman40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MINO-1 - ANIGN=15 -MODE=LOCAL -OUTFWT=ppto -NORM=ext
-HEAPSIZE=500 -MINILEN=0 -MAXLEN=2000000000 -HOST=abss02h
-USER=US09827854 @CGN 1 1 2326 @runat 14062006 081838 26978 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published Applications NA Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
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12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
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15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
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                                                                                             June 14, 2006, 21:46:34; Search time 129.918 Seconds (without alignments) 2553.658 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
             GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                   - nucleic search, using frame plus p2n model
                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                     18892170 seqs, 6143817638 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                   1 MKVLWAALLVTFLAGCQA 18
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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92
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Maximum DB seq length: 2000000000
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Match Length DB
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Database :

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Best Local Similarity:
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                Query Match:
DB:
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| Sequence 8950, Application US/10995561
| Sequence 8950, Application US/1099561
| Publication No. US20050272054A1
| Publication No. US20050272054A1
| GRNERAL INFORMATION: GRETIC POLYMORPHISMS ASSOCIATED WITH
| TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
| TITLE OF INVENTION: DETECTION AND USES THEREOF
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Matches:
Conservative:
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Matches:
Conservative:
Mismatches:
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ORGANISM: Homo sapiens
US-10-995-561-8950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
US-10-741-601-3278
                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
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US-10-741-601-3278
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Pred. No.:
                                    Alignment Scores:
Pred. No.:
   US-09-391-104-4
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RESULT 5
US-10-696-639-2937
US-10-696-639-2937
Sequence 2937, Application US/10696639
Sequence 2937, Application US/1069639
Sequence 2937, Application No. US20050037439A1
GENERAL INFORMATION:
APPLICANT: Pharmacia Corporation
APPLICANT: Bourner, Maureen J.
TITLE OF INVENTION: DIFFERNITALLY EXPRESSED GENES INVOLVED IN CANCER, THE
FILE REFERENCE: 0.1040/1
CURRENT APPLICATION NUMBER: US/10/696,639
FILE REPERENCE: 2003-10-29
FRIOR APPLICATION NUMBER: 60/422,176
FRIOR APPLICATION NUMBER: 60/422,176
FRIOR FILING DATE: 2002-10-29
NUMBER OF SEQ ID NOS: 3114
SEQ ID NO 2937
LENGTH: 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Catched, Kim
APPLICANT: Pechted, Kim
APPLICANT: Agostino, Michael J.
APPLICANT: Howes, Steven H.
APPLICANT: Howes, Steven H.
APPLICANT: Gesnick, Richard J.
APPLICANT: Gulukota, Kamalakat
APPLICANT: Graham, James R.

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Mismatches:
Indels:
                                                                                                                                                                US-09-827-854A-13 (1-18) x US-10-995-561-8950 (1-201
Mismatches:
Indels:
Gaps:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09823245A; Publication No. US20020039760A1; GENERAL INFORMATION, APPLICANT: Wong, Gordon G.; APPLICANT: Clark, Hilary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.: 2.63e-06
Score: 92.00
Percent Similarity: 100.0$
Query Match: 100.0$
100.0%
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ORGANISM: homo sapiens
FEATURE:
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CORGANISM: Homo sapiens
US-09-823-245A-7
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us-09-827-854a-13.p2n.rnpbm

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TYPE: DNA ORGANISM: Homo sapiens
         ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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US-09-964-824A-374/c
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Pred. No.:
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Sequence 2936, Application US/10696639

Fublication No. US20050037439A1

GENERAL INFORMATION:
APPLICANT: Pharmacia Corporation
APPLICANT: Bourner, Maureen J.
TITLE OF INVENTION: DIFFRENTIALLY EXPRESSED GENES INVOLVED IN CANCER, THE
TITLE OF INVENTION: DIFFRENTIALLY EXPRESSED GENES INVOLVED IN CANCER, THE
TITLE OF INVENTION: DIFFRENTIALLY EXPRESSED GENES INVOLVED IN CANCER, THE
CURRENT APPLICATION NUMBER: US/10/696,639
CURRENT FILING DATE: 2003-10-29

PRIOR PELICATION NUMBER: 60/422,176

PRIOR FILING DATE: 2002-10-29

NUMBER OF SEQ ID NOS: 3114

SEQ ID NO 2936

LENGTH: 441
                                                                                                                                                                                                                                                                                 56 ATGAAGGTTCTGTGGGGCTGCTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 109
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Sequence 8875, Application US/09918995

Publication No. US20030073623A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR APPLICATION NUMBER: US/09/235,076

SPRIOR APPLICATION NUMBER: US/09/235,076

SPRIOR FILING DATE: 2001-07-30

SEQ ID NOS: 38054

SEQ ID NOS: 38054

SEQ ID NO 8875

LENGTH: 445

TYPE: DNA
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Matches:
Conservative:
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Indels:
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Matches:
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100.0%
100.0%
; NAME/KEY: misc_feature
; LOCATION: (339]..(412)
; OTHER INFORMATION: n=unknown
US-10-696-639-2937
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CORGANISM: homo sapiens
US-10-696-639-2936
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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Sequence 374, Application US/09964824A

Sequence 374, Application US/09964824A

Sequence 374, Application US/000102531A1

GENERAL INFORMATION:
THE OF INVENTION: Set and Therapeutic Screening Using Signa TITLE OF INVENTION: Set and TITLE OF INVENTION UNBER: US/09/964,824A

CURRENT FILING DATE: 2001-09-27

PRIOR PELLING DATE: 2000-09-28

PRIOR PELLING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US/60/236,032

PRIOR APPLICATION NUMBER: US/60/236,032

PRIOR APPLICATION NUMBER: US/60/236,028

PRIOR APPLICATION NUMBER: 105/60/236,028

PRIOR APPLICATION NUMBER: 105/60/236,032

PRIOR APPLICATION NUMBER: 105/60/236,033

PRIOR APPLICATION NUMBER: 105/60/236,033
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
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APPLICANT: Horne, Darci T.; APPLICANT: Vockley, Joseph G. APPLICANT: Scherf, Uwe APPLICANT: Gene Logic, Inc.
PEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(445)
OTHER INFORMATION: n = A,T,C or US-09-918-995-8875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature

// LOCATION: (1)...(478)

// OTHER INFORMATION: n=a,t,g or c

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Gaps:

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RESULT: 11

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RESULT: 11

RESULT: 11

RESULT: 12

RESULT: 14

RESULT: 15

RESULT: 14

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RESULT: 15

RESULT
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   Matches:
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Mismatches:
Indels:
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; OTHER INFORMATION: n=a,t,g or
US-10-843-641A-1016
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ORGANISM: Homo sapiens
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Best Local Similarity:
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US-09-73-367C-1016/C

US-09-73-367C-1016/C

Sequence 1016, Application US/09873367C

Publication No. US20030165839A1

GENERAL INFORMATION:

APPLICANT: Soppet, Daniel

APPLICANT: Endress, Gregory

BRIOR PILING DATE: 2000-01-01

PRIOR PILING DATE: 2000-11-01

APPLICANT: MANUMER OF SEQ ID NOS: 1067

SEQUIMARE OF SEQ ID NOS: 1067

APPLICANT: MANUMER OF SEQ ID NOS: 1067
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TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer FILE REPERENCE: 44921-5028-WO CURRENT APPLICATION NUMBER: US/09/880,107 CURRENT FILING DATE: 2001-06-14 PRIOR PAPLICATION NUMBER: US 60/211,379 PRIOR APPLICATION NUMBER: US 60/211,379 PRIOR APPLICATION NUMBER: US 60/237,054 PRIOR APPLICATION NUMBER: US 60/237,054 PRIOR FILING DATE: 2000-10-02 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 2491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Genbank Accession No. US20020142981A1 N33009
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LOCATION: (1)..(478)

7 OTHER INDEMATION: n = a or c or g or

US-09-880-107-2491
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CTHER INFORMATION: n=a,t,g or
US-09-873-367C-1016
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NAME/KEY: misc_feature
LOCATION: (1)...(478)
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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ORGANISM: Homo sapiens
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Best Local Similarity:
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Pred. No.:
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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 8447
SOFTWARE: Patentin version 3.0
SEQ ID NO 1016
LENGTH: 478
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Conservative:
Mismatches:
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US-10-843-641A-5677/c
; Sequence 5677, Application US/10843641A
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478

Length:

3.16e-06

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APPLICANT: VOSE, Edward Z.
APPLICANT: ACINC, VOSE, Edward Z.
APPLICANT: Shong, Mei
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METH
FILE OF INVENTION: THEAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METH
FILE OF INVENTION: THEAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METH
FILE OF INVENTION: THEAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METH
FILE OF INVENTION NUMBER: 60/31151
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/310, 795
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2002-08-08
PRIOR FILING DATE: 2002-04-16
PRIOR FILING DATE: 2002-04-16
PRIOR FILING DATE: 2002-04-16
PRIOR FILING DATE: 2002-04-16
PRIOR FILING DATE: 2002-06-15
PRIOR APPLICATION NUMBER: 60/311, 979
PRIOR FILING DATE: 2002-06-15
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Matches:
Conservative:
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Indels:
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APPLICANT: Anderson, David W.
APPLICANT: Beldog, Ferenc L.
APPLICANT: Beldog, Ferenc L.
APPLICANT: Casman, Stacie J.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Gangolli, Esha A.
APPLICANT: Gorman, Linda
APPLICANT: Gorman, Linda
APPLICANT: Lepley, Denise M.
APPLICANT: Lepley, Denise M.
APPLICANT: Pena, Carol A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-211-689-29
. Sequence 29, Application US/10211689
. Publication No. US20030232347A1
. GENERAL INFORMATION:
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 950
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 976
LENGTH: 583
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Patturajan, Meera
Rieger, Daniel K.
Shimkets, Richard A.
Smithson, Glennda
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Vernet, Corine A. M.
Voss, Edward Z.
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; LOCATION: (100)..(423)
US-10-302-172-876
                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
Query Match:
DB:
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Publication No. US20040053250A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ate, Aidong J.
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20040053250A1e1 Arginine-rich Protein-like Nucleic Acids an TITLE OF INVENTION: No. US20040053250A1e1 Arginine-rich Protein-like Nucleic Acids an TITLE OF INVENTION: No. US20040053250A1e1 Arginine-rich Protein-like Nucleic Acids an TITLE OF INVENTION: NO. US20040053250A1e
FILE REFERENCE: 803 LCNCP
CURRENT FILING DATE: 2002-01-1-21
PRIOR APPLICATION NUMBER: US 10/225, 251
PRIOR PELING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 09/799,451
                                          GENERAL INCRMATION:

GRAPLICANT: Avalon Pharmaceuticals, Inc.

TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using TITLE OF INVENTION: Signature Gene Sets
FILE REPRENCE: 689290-189

CURRENT FILING DATE: 2004-05-12

FRIOR APPLICATION NUMBER: US/09/9813,367

PRIOR FILING DATE: 2001-06-05

PRIOR FILING DATE: 2001-09-18

PRIOR FILING DATE: 2001-09-18

PRIOR FILING DATE: 2001-09-25

PRIOR FILING DATE: 2001-09-25

PRIOR PAPLICATION NUMBER: US/09/962,436

PRIOR FILING DATE: 2001-09-25

PRIOR PELING DATE: 2001-09-25

PRIOR APPLICATION NUMBER: US/09/962,832

PRIOR FILING DATE: 2001-09-25

PRIOR PELING DATE: 2001-09-25

PRIOR FILING DATE: 2001-09-25

PRIOR FILING DATE: 2001-09-25

PRIOR PELING DATE: 2001-09-25

PRIOR FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-09-28

PRIOR PELICATION NUMBER: US/09/969,708

PRIOR FILING DATE: 2001-10-03

PRIOR FILING PATE: 2001-10-03

PRIOR FILING DATE: 2001-10-03
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COTHER INFORMATION: n=a,t,g or c
US-10-843-641A-5677
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PRIOR APPLICATION NUMBER: 60/380,970
PRIOR FILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: 60/311,979
PRIOR PILING DATE: 2001-08-13
PRIOR FILING DATE: 2002-05-16
PRIOR PILING DATE: 2002-05-16
PRIOR PILING DATE: 2001-09-21
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 132
SOFTWARE: CURASEQLIST Version 0.1
SEQ ID NO 41
LENGTH: 709
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ORGANISM: Homo sapiens
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, LOCATION: (2)
US-10-211-689-41
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APPLICANT: Spytek, Kimberly A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Vernet, Corine A. M.
APPLICANT: Shong, Mei
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD FILE REPERBURES: 21402-416B
CURRENT APPLICATION NUMBER: US/10/211,689
CURRENT FILING DATE: 2003-01-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/381,030
PRIOR FILING DATE: 2002-05-16
PRIOR FILING DATE: 2002-05-16
PRIOR FILING DATE: 2001-09-21
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 132
SOFTWARE: CuraseqList version 0.1
SEQ ID NO 29
LENGTH: 684
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Matches:
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PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-08
PRIOR PILING DATE: 2001-08-08
PRIOR PILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/311,292
PRIOR PILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/361,159
PRIOR APPLICATION NUMBER: 60/361,159
PRIOR APPLICATION NUMBER: 60/361,159
PRIOR APPLICATION NUMBER: 60/361,159
PRIOR PILING DATE: 2002-02-28
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; Sequence 41, Application US/10211689
; Publication No. US20030232347A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Alsobrook, John II
APPLICANT: Anderson, David W.
APPLICANT: Boldog, Ferenc L.
APPLICANT: Burgess, Catherine B.
APPLICANT: Casman, Stacte J.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Gangolli, Esha A.
APPLICANT: Granan, Linda
APPLICANT: Khramstov, Nikolai V.
APPLICANT: Khramstov, Nikolai V.
APPLICANT: Lepley, Denlse M.
APPLICANT: Pena, Carol A.
APPLICANT: Pena, Carol A.
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Rieger, Daniel K.
Shimkets, Richard A.
Smithson, Glennda
Spytek, Kimberly A.
Vernet, Corine A. M.
Voss, Edward Z.
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; LOCATION: (18)..(599)
US-10-211-689-29
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25053, A 27233, A 27234, A 21037, A 210333, A 24008, A 2653, Ap 22166, A 490, App 1895, A 1895, A 412, A

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Minimum DB Maximum DB

Searched:

7083, Ap 14774, A

79433, A 12686, A 18815, A 13080, A 22075, A

Sequence Seq

2087, Ap 8455, Ap 18066, A 36046, A 20458, A

1429, Ap 24160, A 1127, Ap 17714, A

Sequence Sequence

Sequence Sequence

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Run on:

Sequence:

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Sequence 1, Application US/10524021

Sequence 1, Application US/10524021

Bublication No. US20060099590A1

GENERAL INFORMATION:

APPLICANT: NAGOYA INDUSTRIAL SCIENCE RESEARCH INSTITUTE
APPLICANT: VAMADA, Yoshiji

APPLICANT: YAMADA, Yoshiji

TITLE OF INVENTION: Method for diagnosing a risk of restenosis after percutaneous of TITLE OF INVENTION: intervention

FILE REFERENCE: C0200501

CURRENT APPLICATION NUMBER: US/10/524,021

CURRENT FILING DATE: 2005-02-09

PRIOR PILING DATE: 2002-08-09

PRIOR FILING DATE: 2002-08-09

NUMBER OF SEQ ID NOS: 67

SOFTWARE: PatentIn version 3.1

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US-10-449-902-24008

US-10-449-902-2153

US-10-449-902-2153

US-10-449-902-2185

US-10-449-902-18852

US-10-449-902-18852

US-10-449-902-18852

US-10-449-902-1886

US-10-449-902-1083

US-11-27-529-80129

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US-10-524-021-1
       Query Match:
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Sequence 18081, A
Sequence 2323, A
Sequence 64, Appl
Sequence 17095, A
Sequence 28183, A
Sequence 28183, A
Sequence 10702, A
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2035.043 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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                                                                                                                                                               ; Search time 3.12303 Seconds
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-649-902-18081
US-11-189-279-64
US-11-189-279-64
US-10-519-35-37
US-10-649-902-17095
US-10-449-902-10702
US-10-449-902-10702
US-10-449-902-10702
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                             June 14, 2006, 22:11:12
                                                                                                                                                                                                                                                                                                      1 MKVLWAALLVTFLAGCQA 18
                                                                                                                                                                                                                                                                                                                                                                      Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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seq length: 200000000
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Match 1
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447.8
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Database :

Result No.

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US-10-49-902-17095
US-10-449-902-17095
US-10-449-902-17095

Publication No. US20060123505A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bio-oriented Technology Research Advancement Institute of Physical and Chemical Research.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: The Institute of Physical and Chemical Research.
TILE REPRENCE: MOA-A0205Y1-US
FILE REPRENCE: MOA-A0205Y1-US
FILE REPRENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
PRIOR FILING DATE: 2002-203-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR PRILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56/91
SEQ ID NO 17095

EASTWARE: Patentin Ver. 2.1
SEQ ID NO 17095
                                                               1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
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  US-09-827-854A-13 (1-18) x US-10-953-349-22323 (1-1503)
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                                                                                                                                                                  Sequence 64, Application US/11189279;
Publication No. US20060115829A1
GENERAL INFORMATION:
APPLICANT: MAO, LI
APPLICANT: MAO, LI
APPLICANT: MAO, AIE
APPLICANT: LUO, WANG
TITLE OF INVENTION: A METHOD OF TREATING CANCER
FILE REFERENCE: UTXC:875US
CURRENT FILING DATE: 2005-07-26
PRIOR APPLICATION NUMBER: 60/598,554
PRIOR APPLICATION UNMBER: 60/598,554
PRIOR APPLICATION NUMBER: 60/598,554
PRIOR APPLICATION NUMBER: 60/598,554
NUMBER OF SEQ ID NOS: 69
SOFTWARRE: PATENTING DATE: 2004-08-03
SOFTWARRE: PATENTING DATE: 2004-08-03
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Matches:
Conservative:
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PUBLICATION INPORMATION:
DATABASE ACCESSION NUMBER: AK067558
DATABASE BUTRY DATE: 2001-12-06
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Best Local Similarity:
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LENGTH: 118899
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Pred. No.:
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Publication No. US20060107345A1

GENERAL INFORMATION:
TITLE OF INVENTION: BEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: BECONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
                                                                                                                    Sequence 18081. Application US/10449902

Sequence 18081. Application US/10449902

Publication No. US20060123505A1

GENERAL INFORMATION:

APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.

TITLE OF INVENTION: FULL-ENGYLOUS

FILE REFERENCE: MOA-A0205Y1-US

CURRENT FILING DATE: 2003-05-29

PRIOR FILING DATE: 2003-05-29

PRIOR PLICATION NUMBER: UF 2002-3059

PRIOR PLICATION NUMBER: UF 2002-383870

PRIOR PLING DATE: 2002-12-11

NUMBER OF SEQ ID NOS: 56791

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 18081

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458 GITCTGTGGGTTGCTTTGTTACTATGTTTTTTGTTCATGT 499
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Mismatches:
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DATABASE ACCESSION NUMBER: AK068492
DATABASE ENTRY DATE: 2001-12-06
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ORGANISM: Oryza sativa
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Best Local Similarity:
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Best Local Similarity:
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LENGTH: 1503
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LOCATION: (5363)..(5363)
OTHER INFORMATION: n = a or c or g or t
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                                                               NAME/KEY: misc feature
LOCATION: (109094)..(109094)
OTHER INFORMATION: n = a or c or
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LOCATION: (109125)..(109125)
OTHER INFORMATION: n = a or c or
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LOCATION: (119024)..(119052)
OTHER INFORMATION: n = a or c or
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LOCATION: (119053)..(119112)
OTHER INFORMATION: n = a or c or
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NAME/KEY: misc_feature
LOCATION: (142137)..(142137)
OTHER INFORMATION: n = a or c or
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LOCATION: (142063)..(142063)
OTHER INFORMATION: n = a or c or
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LOCATION: (142967)...(142967)
OTHER INFORMATION: n = a or c or
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LOCATION: (143077)...(143077)
OTHER INFORMATION: n = a or c or
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LOCATION: (143506)..(143506)
OTHER INFORMATION: n = a or c or
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LOCATION: (143629)..(143629)
OTHER INFORMATION: n = a or c or
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LOCATION: (118900)..(118900)
OTHER INFORMATION: n = a or c
      LOCATION: (108055)..(108055)
OTHER INFORMATION: n = a or c
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LOCATION: (141674)..(141674)
OTHER INFORMATION: n = a or
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LOCATION: (119115)..(119121)
OTHER INFORMATION: n = a or
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LOCATION: (119123)..(119123)
OTHER INFORMATION: n = a or
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LOCATION: (143587)..(143587)
OTHER INFORMATION: n = a or
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LOCATION: (149079)..(149079)
OTHER INFORMATION: n = a or
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NAME/KEY: misc_feature
LOCATION: (8080)..(8080)
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                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cavarec, Laurent
APPLICANT: Chumakov, 11ya
APPLICANT: Chumakov, 11ya
APPLICANT: Chumakov, 11ya
APPLICANT: Destenaves, Benoit
APPLICANT: Destenaves, Benoit
APPLICANT: Bestenaves, Cacherine
APPLICANT: Blias, Isabelle
APPLICANT: Blias, Isabelle
APPLICANT: RISALING: TRABATMENT OF MENTAL DISORDERS
TITLE OF INVENTION: TRABATMENT OF MENTAL DISORDERS
FILE REFERENCE: G-194USO3PCT
CURRENT APPLICATION NUMBER: US/10/519,335
CURRENT FILING DATE: 2004-12-22
FRIOR APPLICATION NUMBER: US 60/391,359
FRIOR APPLICATION NUMBER: US 60/391,359
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PATENT OF VERY NOS: 47
SOFTWARE: PATENT OF VERY NOS: 47
                                                                                                                                                                                                  1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
                                                                                                                                 US-09-827-854A-13 (1-18) x US-10-449-902-17095 (1-2553)
Matches:
Conservative:
Mismatches:
Indels:
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NAME/KEY: misc_feature
LOCATION: (982\overline). (982\overline)
OTHER INFORMATION: n = a or c or g or t
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LOCATION: (99743)..(99743)
OTHER INFORMATION: n = a or c or g or t
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OTHER INFORMATION: n = a or c or g or t
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LOCATION: (61110) ..(61110)
OTHER INFORMATION: n = a or c or g or
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LOCATION: (98209)..(98209)
OTHER INFORMATION: n = a or c or g or
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LOCATION: (98210)..(98210)
OTHER INFORMATION: n = a or c or g or
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LOCATION: (98211)..(98211)
OTHER INFORMATION: n = a or c or g
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; Sequence 37, Application US/10519335
; Publication No. US2006009210A1
; GENERAL INFORMATION:
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LOCATION: (98207)..(98207)
OTHER INFORMATION: n = a or
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51.1%
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                    Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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Best Local Similarity:
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                                NAME/KEY: misc feature
LOCATION: (10296)..(10296)
OTHER INFORMATION: n = a or c or g or
                                                                            FEATURE:
NAME/KEY: misc feature
LOCATION: (14528)
OTHER INFORMATION: n = a or c or g or
FEATURE:
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LOCATION: (15457) .. (15457)
OTHER INFORMATION: n = a or c or
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LOCATION: (16316)..(16316)
OTHER INFORMATION: n = a or c
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LOCATION: (16397)..(16397)
OTHER INFORMATION: n = a or c
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LOCATION: (56012)..(56012)
OTHER INFORMATION: n = a or c
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LOCATION: (57662)..(57662)
OTHER INFORMATION: n = a or
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LOCATION: (125441)..(125605)
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LOCATION: (15336)..(15336)
OTHER INFORMATION: n = a or
                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (16288)..(16288)
OTHER INFORMATION: n = a or
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OTHER INFORMATION: n = a or
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LOCATION: (99546)..(99723)
OTHER INFORMATION: exon 5
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LOCATION: (96310)..(96422)
OTHER INFORMATION: exon 4
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OTHER INFORMATION: exon 2
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OTHER INFORMATION: exon 1
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OTHER INFORMATION: exon 1
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LOCATION: (16306)..(163
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Score:
Percent Similarity:
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LOCATION: (936
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y Sequence 10702, Application US/10449902

| Sequence 10702, Application US/10449902
| Publication No. US20060123505A1
| GENERAL INFORMATION:
| APPLICANT: National Institute of Agrobiological Sciences.
| APPLICANT: The Institute of Physical and Chemical Research.
| APPLICANT: The Institute of Physical and Chemical Research.
| APPLICANT: Proundation for Advancement of International Science.
| TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
| FILE REFERENCE: MOA-A0205Y1-US
| CURRENT FILING DATE: 2002-05-30
| PRIOR FILING DATE: 2002-05-30
| PRIOR PELICATION NUMBER: UP 2002-203269
| PRIOR FILING DATE: 2002-12-11
| NUMBER OF SEQ ID NOS: 56791
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 10702
| LENGTH: 1371
                                                                                                                                                                                                                                          US-10-449-902-28383/c

US-10-449-902-28383/c

Sequence 28383 Application US/10449902

Publication No. US20060123505A1

GENERAL INFORMATION:

APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: Bio-oriented Technology Research Advancement Institution.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.

TILE REFERENCE: MOA-A0205Y1-US

FILE REFERENCE: MOA-A0205Y1-US

CURRENT FILING DATE: 2003-05-30

PRIOR PRING DATE: 2003-05-30

PRIOR PRING DATE: 2002-12-11

NUMBER OF SEQ ID NOS: 56791

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 28383

LENGTH: 586
                                                                                                                                                                         151567 AGGTTGTTGGTGGCGGCGATGGCAATGATGTTCTCAGCCGGGTGCCAGGCC 151517
                                                                                                                                    2 LysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
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                                                                                            US-09-827-854A-13 (1-18) x US-10-519-335-37 (1-151830)
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Indels:
Mismatches:
Indels:
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Matches:
                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK103825
DATABASE ENTRY DATE: 2002-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.9
44.00
71.4%
50.0%
52.9%
48.9%
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Pred. No.:
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Phygical and Chemical Research.
APPLICANT: The Institute of Phygical and Chemical Research.
APPLICANT: The Institute of Phygical and Chemical Research.
ITILE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
PRIOR FILING DATE: 2003-05-29
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-012-11
NUMBER OF SEQ ID NOS: 56/791
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Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1054 GTCATGTGGACGCCGTCCCAGTTGACGTACTTGGCCGGCTGC 1013
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Mismatches:
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Mismatches:
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Matches:
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Publication No. US20060123505A1
GENERAL INFORMATION:
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK108050
DATABASE ENTRY DATE: 2002-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AKO59168
DATABASE ENTRY DATE: 2001-12-06
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44.00
71.4$
50.0$
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Best Local Similarity:
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Best Local Similarity:
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Pred. No.:
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APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Toundation for Advancement of International Science.
ITLE REPERRINCE: MOA-AO20571-US
FILE REPERRINCE: MOA-AO20571-US
CURRENT FILING DATE: 2003-05-29
PRIOR FILING DATE: 2003-05-29
PRIOR PLING DATE: 2003-05-30
PRIOR PLING DATE: 2002-05-30
PRIOR PLING DATE: 2002-05-30
PRIOR PLING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SEQ ID NO 13084
LENGTH: 2794
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Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
FRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PACENTIN VET: 2.1
SOFTWARE: AECHLIN VET: 2.1
SOFTWARE: 2618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 TrpAlaAlaLeuLeuValThrPheLeuAlaGly
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                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK100495
DATABASE ENTRY DATE: 2002-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK110432
DATABASE ENTRY DATE: 2001-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.00
81.8%
72.7%
47.8%
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
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Sequence 21037, Application US/10449902
| Sequence 21037, Application US/10449902
| Publication No. US20060123505A1
| GENERAL INFORMATION:
| APPLICANT: National Institute of Agrobiological Sciences.
| APPLICANT: Bio-oriented Technology Research Advancement Institution.
| APPLICANT: Foundation for Advancement of International Science.
| APPLICANT: Foundation for Advancement of International Science.
| APPLICANT: Foundation for Advancement of International Science.
| TITLE OF INVENTY APPLICATION NUMBER: US/10/449,902
| CURRENT APPLICATION NUMBER: US/10/449,902
| PRIOR PILING DATE: 2002-05-30
| PRIOR FILING DATE: 2002-05-30
| PRIOR FILING DATE: 2002-12-11
| NUMBER OF SEQ ID NOS: 56791
| SEQ ID NO 21037
| LEGITLE OF SEQ ID NOS: 56791
| SEQ ID NO 21037
     Sequence 27239, Application US/10449902

Publication No. US20060123505A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
The Institute of Agrobiological Sciences.
APPLICANT:
TITLE OF INVENTION:
TITLE OF INVENTION:
Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGIP PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A02051-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 27239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 TrpAlaAlaLeuLeuValThrPheLeuAlaGlyCys 16 |||||| ::: ||||||| 1532 TGGGCCATGATGTGCCAGACCTTCCTATCGGGATGC 1567
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Mismatches:
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Matches:
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ORGANISM: OFYZA SALIVA
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK071336
DATABASE BNTRY DATE: 2001-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK102681
DATABASE ENTRY DATE: 2002-08-28
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58.3%
47.8%
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Best Local Similarity:
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Pred. No.:
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DB:
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2260

Length:

145

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Sequence 24008, Application US/10449902

| Sequence 24008, Application US/10449902
| Publication No. US20060123505A1 |
| GENERAL INFORMATION: |
| APPLICANT: National Institute of Agrobiological Sciences. |
| APPLICANT: Bio-oriented Technology Research Advancement Institution. |
| APPLICANT: Foundation for Advancement of International Science. |
| APPLICANT: Foundation for Advancement of International Science. |
| APPLICANT: Foundation for Advancement of International Science. |
| TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF |
| FILE REFERENCE: MOA-A0205Y1-US |
| CURRENT FILING DATE: 2002-05-30 |
| PRIOR APPLICATION NUMBER: UP 2002-203269 |
| PRIOR FILING DATE: 2002-05-30 |
| PRIOR FILING DATE: 2002-12-11 |
| NUMBER OF SEQ ID NOS: 56791
                                                                                                                                                                                                                                                                                                                                      Sequence 15333, Application US/10449902

Publication No. US20060123505A1

GENERAL INFORMATION:

APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: Bio-oriented Technology Research Advancement Institution.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: The Institute of Physical and Chemical Research.

TITLE OF INVENTION: FOLIAL-LENGTH PLANT CDNA AND USES THEREOF

FILE REFERENCE: MOA-A02051-US

CURRENT APPLICATION NUMBER: US/10/449,902

CURRENT PILING DATE: 2002-05-30

PRIOR FILING DATE: 2002-05-30

PRIOR FILING DATE: 2002-12-11

NUMBER OF SEQ ID NOS: 56791

SECONTANE: Patentin Ver. 2.1
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1401 ATGABABACTTGTGGCAGTTGGTGTAGTTGATATCCTTACTABGTGCCTGTCABGCA 1457
                                                                                                                                                                                                      1 MetLysValLeuTrpAlaAlaLeu---LeuValThrPheLeuAlaGlyCysGlnAla 18
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                                                                                                                                                       US-09-827-854A-13 (1-18) x US-10-449-902-21037 (1-2260)
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Matches:
Conservative:
Mismatches:
Indels:
                          Conservative:
Mismatches:
Matches:
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK065861
DATABASE ENTRY DATE: 2001-12-06
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  43.50
73.7$
47.4$
47.3$
                          Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
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LENGTH: 2265
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| JENGTH: 2392
| JENGTH: 2392
| TYPE: DNA
| TYPE: DNA
| PEATURE:
| NAME/KEY: misc_feature
| CATATION: (1106)
| OTHER INFORMATION: "n"=any one base of a, t, c, or g
| DATABASE ENTRY DATE: 2002-08-28
| JOATABASE ENTRY DATE: 2002-08-29
| JOATABASE ENTRY DATE: 2002-08-28
| JOATABASE ENTRY DATE: 2002
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Search completed: June 14, 2006, 22:15:10 Job time: 9.12303 secs

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